**REMARKS**

**I. Status of the Claims and Amendment**

Claims 2, 4, 5, 9, 13, 16-19, 23, 28-30 and 32-35 are all the claims pending in the

application. Claims 1, 3, 6-8, 10-12, 14-15, 20-22, 24-27, 31, and 36-37 were previously

canceled. Claims 16-19, 23, 28-30, and 32-35 are withdrawn as being directed to non-elected

inventions. Claim 2 has been amended to further clarify that "oligonucleotides having the

sequence set forth in SEQ ID Nos: 117, 127, 137, 138, 147, 169, 178, 225, 231, 272, 278, 310,

329, 335, 339, 346, 352, 361, 386, 387, 399, 420, 429, 469, 472, or 477 may only be replaced by

an oligonucleotide having a sequence entirely complementary to the one of said oligonucleotides

being replaced or by an oligonucleotide having at least 80% identity to the one of said 351

oligonucleotides being replaced." Support for the amendment to claim 2 may be found

throughout the specification, for example in the original claims.

In addition, the specification at Table 1a has been amended to correct an apparent

typographical error with regard to SEQ ID NO:. 499. Namely, SEQ ID NO: 499 in Table 1a has

been corrected to SEQ ID NO: 501. Further, the number of nucleotides has been corrected to

"464" instead of "421". Similarly, SEQ ID NO: 500 has been corrected to SEQ ID NO: 499.

These amendments are consistent with the previous amendment filed March 11, 2010 to SEQ ID

NOs: 500 and 501 at pages 277-278 of the Substitute Specification.

The third paragraph at page 277 of the Substitute Specification has also been amended to

correct the apparent error to the number of nucleotides for SEQ ID NO: 500 so that the

nucleotide number is "556" instead of "559". Support for the correction to this apparent error is

provided by the Sequence Listing as evidenced by the BLAST alignment provided herewith.

Further, a new Substitute Sequence Listing is submitted herewith to correct an apparent error with SEQ ID NO:420.  Support for the correction to SEQ ID NO: 420, may be found on page 246 of the Substitute Specification filed October 3, 2008 and original Sequence ID 1205 on pages 249-250 of the as-filed specification..  Namely, an error occurred in which 59 nucleotides from the 3' end were not listed.  The new Substitute Sequence Listing submitted herewith corrects this apparent error.

No new matter is added.

**II. Response to the Objection to the Specification**

The Examiner objects to the Amendments filed March 11, 2010, October 3, 2008, and July 6, 2009, under 35 U.S.C. § 132(a) as allegedly introducing new matter into the disclosure.

(a) The first objection concerns the amendment to SEQ ID NO: 36 to indicate that it has 527 nucleotides, rather than the 258 nucleotides previously recited.

(b) The Examiner asserts that the previous amendment to the specification concerning the sequence listing and identification of sequences by SEQ ID NOs is new matter.  The Examiner asserts that the response of March 11, 2010 provided a sequence alignment in an attempt to demonstrate that no new matter was added by previous amendments.  As detailed in the Office Action on pages 3-7 and 16, the Examiner noted that the alignment previously submitted showed that many of the sequences (SEQ ID NOs) are shorter than the corresponding originally submitted sequences.

With regard to (a), Applicants note that SEQ ID NO:36 contains 527 nucleotides, as determined by counting the nucleotides.  In the application as filed this sequence was sequence No. 364.  Whilst it was stated that the sequence had 528 nucleotides in the application as filed,

this was an error. This correction is further supported by the new Substitute Sequence Listing

which is consistent with the disclosure in the Substitute Specification and as-filed specification.

With regard to (b), Applicants have identified the errors in the previous alignment

submission and herewith provide a new alignment to demonstrate that the sequences in the

Substitute Specification filed October 3, 2008 (which are consistent with the Substitute Sequence

Listing of May 1, 2006) and the sequences in the "PCT application"[1] (which is the as-filed

specification of May 19, 2005) are identical and the same.

In this respect, Applicants note that the errors presented in the BLAST alignments

previously submitted were due to the propensity of the BLAST program to trim sequences

(particularly after "N" bases) so that sequence identity was reported over a smaller region than

the full length sequence, or the program failed to perform an appropriate alignment.

Accordingly, Applicants have revisited each comparison and provide herewith a new

BLAST comparison for each of the sequences. Applicants also submit herewith a table showing

the sequences that were incorrectly aligned and the cause of the error. The sequences not

identified by the Examiner but showing errors are highlighted in the Table in bold. The BLAST

sequence comparisons that have been corrected in the new BLAST comparison are annotated at

the end of the comparison to describe the error that occurred and the remedial measures that were

---

[1] As the Examiner may recall, in the Amendment filed October 3, 2008, Applicants noted that a
Sequence Listing was filed May 1, 2006 containing all the sequences disclosed in the original
specification. The Sequence ID numbers listed in the original specification were not in consecutive
order, starting at 93 and ending at 1495 (with many numbers missing in between). Additionally,
Sequence IDs G6, 61, 490, 892 and 77 appeared at the end of the otherwise numerically increasing
list. Subsequently a Sequence Listing was filed on May 1, 2006 in which the sequences were
presented in a consecutive list of 501 sequences, but the sequences in the specification were
inadvertently not amended at the same time to correspond to the list of 501 sequences. The Substitute
Specification filed October 3, 2008 was merely provided to remedy this matter so that the original
sequences disclosed correspond to the SEQ ID NOs in the Sequence Listing of May 1, 2006.

taken to allow the appropriate comparison to be made. As discussed above, in most cases, the trimmed sequences removed by the BLAST program were reinstated and the comparison across the full length completed. However, in some cases, where the sequences were misaligned, the sequences were compared in portions and the comparisons merged to generate the comparison of the full sequences (e.g., Sequences 313, 326, 673, 686, 1210, 1225 and 1332 as filed).

Thus, the enclosed new BLAST comparison shows 100% identity between the sequences of the application as filed and those submitted in the Substitute Specification filed October 3, 2008.

Withdrawal of the grounds of objection is respectfully requested.

**III.    Response to Enablement Rejection**

Claims 2, 4-5, 9 and 13 remain rejected under 35 U.S.C. § 112, first paragraph, for lack of enablement.

(A) The Examiner asserts that, due to the new matter issues addressed above, it would be unpredictable for one of skill in the art to determine which nucleic acids are informative in the instant method. That is, it appears the claims are asserted to not be enabled due to the amendments to the specification that have resulted in inconsistencies in the disclosure and thus the unpredictability of the claimed invention.

In response, as discussed above, Applicants have amended the specification to correct apparent typographical errors, and submit herewith a new BLAST sequence alignment to show that the sequences in the Substitute Specification filed October 3, 2008 and the sequences in the as-filed specification of May 1, 2005 are the same. The sequence alignment supports Applicants' previous arguments to demonstrate that the specification contains no new matter,

and that the specification enables one of ordinary skill in the art to make and use the claimed

invention.

(B) The Examiner asserts that the use of any fragment of a claimed SEQ ID NO that is (i)

at least 30 nucleotides of the SEQ ID NO being replaced, (ii) at least 30 nucleotides and

completely complementary to the sequence being replaced, or (iii) at least 80% identity to the

sequence being replaced or a fragment thereof, is unpredictable.

First, the Examiner asserts that some SEQ ID NOs are shorter that 30 nucleotides, and

allegedly no guidance is provided as to how they could be replaced by fragments of at least 30

nucleotides. For example, the Examiner points to: SEQ ID NO: 117, which is 28 nucleotides;

SEQ ID NO: 138, which is 4 nucleotides; SEQ ID NO: 225, which is 17 nucleotides; and SEQ

ID NO: 361, which is 12 nucleotides.

Second, the Examiner asserts the specification provides no indication that every or any 30

base fragment of the recited SEQ ID NOs allow detection as the full length sequences taught by

the specification to be indicative of differential expression patterns. Specifically, the Examiner

notes that several sequences have poly adenine regions longer than 30 nucleotides, and that

replacement of the full length claimed nucleic acid sequences with a fragment of the poly

adenine would allow for detection of any nucleic acid sequence with a poly T, such as every

reverse transcribed RNA, but not the specific sequences of the SEQ ID NO. For example, the

Examiner points to: SEQ ID NO: 346 having a stretch of 46 adenines; SEQ ID NO: 335 having a

stretch of 33 adenines; and SEQ ID NO: 429 having a stretch of 33 adenines.

In response, and solely to advance prosecution of the present application, claim 2 has

been amended to recite that "oligonucleotides having the sequence set forth in SEQ ID Nos. 117,

127, 137, 138, 147, 169, 178, 225, 231, 272, 278, 310, 329, 335, 339, 346, 352, 361, 386, 387,

399, 420, 429, 469, 472, or 477 may only be replaced by an oligonucleotide having a sequence

entirely complementary to the one of said oligonucleotides being replaced or by an

oligonucleotide having at least 80% identity to the one of said 351 oligonucleotides being

replaced."

Therefore the claimed invention is enabled and withdrawal of the rejection under 35

U.S.C. § 112, first paragraph, is respectfully requested.

## IV. Conclusion

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

Respectfully submitted,

Eric B. Ives, Ph.D.
Registration No. 50,928

SUGHRUE MION, PLLC
Telephone: (202) 293-7060
Facsimile: (202) 293-7860
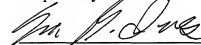
WASHINGTON OFFICE
23373
CUSTOMER NUMBER

Date: December 1, 2010

| Sequence No. as filed | Sequence No. in Sequence Listing | Length | Alignment between Seqs as filed and Oct subs | Error | Missing sequence correct in compared sequences | Cause of error |
|---|---|---|---|---|---|---|
| 308 | 11 | 373 | ID over 371 | Missing "NC" at 3' end | Yes | BLAST |
| 313 | 15 | 554 | ID 170/191 | Misalignment of sequences | Yes | BLAST |
| 326 | 24 | 554 | ID 170/191 | Misalignment of sequences | Yes | BLAST |
| 327 | 25 | 674 | ID 671/671 | Missing "NAT" at 3' end | Yes | BLAST |
| 364 | 36 | 527 | ID 524/524 | Missing "NCA" at 3' end | Yes | BLAST |
| 403 | 66 | 202 | ID 200/200 | Missing "NG" at 3' end | Yes | BLAST |
| 406 | 68 | 644 | ID 641/641 | Missing "NTC" at 3' end | Yes | BLAST |
| 431 | 93 | 131 | ID 126/126 | Missing "NANCA" at 3' end | Yes | BLAST |
| 433 | 95 | 687 | ID 684/684 | Missing "NTC" at 3' end | Yes | BLAST |
| 446 | 102 | 341 | ID 336/336 | Missing "NANAA" at 3' end | Yes | BLAST |
| 469 | 116 | 161 | ID 159/159 | Missing "NA" at 3' end | Yes | BLAST |
| 471 | 117 | 28 | ID 8/8 | Missing "ATCTGCAGGATCCGTCGACT" at 3' end | Yes | BLAST |
| 483 | 128 | 519 | ID 516/516 | Missing "CGN" at 5' end | Yes | BLAST |
| 518 | 155 | 502 | ID 499/499 | Missing "NAT" at 3' end | Yes | BLAST |
| 631 | 232 | 493 | ID 491/491 | Missing "TN" at 5' end | Yes | BLAST |
| 661 | 260 | 256 | ID 253/253 | Missing "NGG" at 3' end | Yes | BLAST |
| 673 | 268 | 683 | ID 127/127 | Missing 547 nucl. at 5' end, "NNNGGGGAA" at 3' end | Yes | BLAST |
| 679 | 272 | 688 | ID 682/682 | Missing "GNANCN" at 5' end | Yes | BLAST |
| 686 | 277 | 603 | ID 28/28 | Misalignment of sequences and majority of the sequence missing | Yes | BLAST |
| 702 | 292 | 709 | ID 705/705 | Missing "GTNN" at 5' end | Yes | BLAST |
| 719 | 306 | 492 | ID 489/489 | Missing "CGN" at 5' end | Yes | BLAST |

| 722 | 309 | 327 | ID 325/325 | Missing "CN" at 5' end | Yes | BLAST |
|------|-----|-----|------------|------------------------|-----|-------|
| 724 | 310 | 273 | ID 272/272 | Missing "N" at 3' end | Yes | BLAST |
| 825 | 332 | 741 | ID 735/735 | Missing "NGGNTT" at 3' end | Yes | BLAST |
| 898 | 360 | 511 | ID 509/509 | Missing "AN" at 5' end | Yes | BLAST |
| 899 | 361 | 16 | ID 13/13 | Missing "TCN" at 5' end | Yes | BLAST |
| 904 | 364 | 649 | ID 648/648 | Missing "N" at 3' end | Yes | BLAST |
| 917 | 375 | 483 | ID 481/481 | Missing "NN" at 5' end | Yes | BLAST |
| 947 | 379 | 646 | ID 641/641 | Missing "NGANG" at 3' end | Yes | BLAST |
| 1071 | 383 | 571 | ID 569/569 | Missing "N" at 5' end and 3' end | Yes | BLAST |
| 1109 | 389 | 601 | ID 594/594 | Missing "NNNNCNN" at 3' end | Yes | BLAST |
| 1125 | 391 | 407 | ID 404/404 | Missing "N" at 5' end and "NT" at 3' end | Yes | BLAST |
| 1193 | 409 | 900 | ID 896/896 | Missing "TNCN" at 5' end | Yes | BLAST |
| 1204 | 419 | 365 | ID 213/213 | Missing from nucleotide 214 at 3' end | Yes | BLAST |
| 1205 | 420 | 299 | ID 241/241 | Missing 58 nucleotides from 3' end | Yes (but missing in Seq. Listing) | BLAST |
| 1210 | 424 | 702 | ID 68/68 | Misaligned and missing large portions from 5' and 3' ends | Yes | BLAST |
| 1220 | 434 | 1354 | ID1343/1343 | Missing "GANNN" at 5' end and "NNNACT" at 3' end | Yes | BLAST |
| 1255 | 442 | 928 | ID 68/68 | Misaligned and missing large portions from 5' and 3' ends | Yes | BLAST |
| **1256** | **443** | 954 | ID 925/925 | Missing "NNNTT.....CCANT" at 3' end | Yes | BLAST |
| **1332** | **445** | 689 | ID 171/191 | Misaligned and missing large portions from 5' and 3' ends | Yes | BLAST |
| **1389** | **473** | 896 | ID 895/895 | Missing "N" at 3' end | Yes | BLAST |

| 1390 | 474 | 350 | ID 347/347 | Missing "TCN" at 5' end | Yes | BLAST |
|------|-----|-----|-----------|-------------------------|-----|-------|
| 1396 | 479 | 912 | ID 909/909 | Missing "NGG" at 3' end | Yes | BLAST |
| 1450 | 486 | 854 | ID 851/851 | Missing "NTC" at 3' end | Yes | BLAST |

# Blast reference

BLASTN 2.2.22+ Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

# Sequence 93 matched with Sequence 1

```
Query=   Sequence ID - 93                    nt:      405
Length=405


   SEQ ID NO: 1              nt:      405

ALIGNMENTS
 Identities = 405/405 (100%), Gaps = 0/405 (0%)

Query  1     GGATCCTGTGGCCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGGAGCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGATCCTGTGGCCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGGAGCC   60

Query  61    CCGGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCCAGCCCTGGCT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCGGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCCAGCCCTGGCT   120

Query  121   GACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGGGAGCAAAGAACG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGGGAGCAAAGAACG   180

Query  181   CCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAGCAGCAGTTGAATGTAA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAGCAGCAGTTGAATGTAA   240

Query  241   TGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACCCGGACAGCCAGGTGACTACC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACCCGGACAGCCAGGTGACTACC   300

Query  301   AGTCCTGGGGACACACTCACCATAAACACATCCCCAGGCAGGACAGATCGGGGAAGGGGT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGTCCTGGGGACACACTCACCATAAACACATCCCCAGGCAGGACAGATCGGGGAAGGGGT   360
```

```
Query  361   GTGTACCAGGCTATGATTTCTCTTGCATTAAAATGTATTATTATT   405
             |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTGTACCAGGCTATGATTTCTCTTGCATTAAAATGTATTATTATT   405
```

# Sequence 108 matched with Sequence 2

```
Query=   Sequence ID - 108                 nt:      550
Length=550


   SEQ ID NO: 2              nt:      550

ALIGNMENTS
 Identities = 550/550 (100%), Gaps = 0/550 (0%)

Query   1    GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACATAGA   60

Query   61   NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   NACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA   120

Query   121  CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAA   180

Query   181  TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCA   240

Query   241  GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAA   300

Query   301  GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCAC   360

Query   361  CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGG   420

Query   421  CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CCACGGCCACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTNTACCCAACCAGGGCCC   480
```

```
Query  481  CGGGGCCTGTTATGTCAAACTGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGGGGCCTGTTATGTCAAACTGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGT  540

Query  541  CTCTTTCTCC  550
            ||||||||||
Sbjct  541  CTCTTTCTCC  550
```

# Sequence 110 matched with Sequence 3

```
Query=   Sequence ID 110
Length=423


   SEQ ID NO: 3

ALIGNMENTS
 Identities = 423/423 (100%), Gaps = 0/423 (0%)

Query  1    ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGGCCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGGCCTG  60

Query  61   CTTCATTAAGAAGCTgggggtagggtgggggtggggAGAACACTTAACAACATGGGGACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACATGGGGACC  120

Query  121  AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGAGCAGCCAGGTGA  180

Query  181  GGCTCTCTAGTTTAATAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGCTCTCTAGTTTAATAAAAATCATGGAAAGACTCTTAATGCAGACTCTTCTTAAGTGTT  240

Query  241  AATAGGGATTTTTTCAGCTTATTTTGGTTGCAGTTTCCAATTTTTAAAAATGTTGAGGTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATAGGGATTTTTTCAGCTTATTTTGGTTGCAGTTTCCAATTTTTAAAAATGTTGAGGTA  300

Query  301  ATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGATGCATTAGTGTTGAACCAATGCTTT  360

Query  361  CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCATGTCTCAATTCTTTGTATATGCATTCTTTTCAGATGTATTAAACAAACAAAAACCC  420

Query  421  TTC   423
            |||
Sbjct  421  TTC   423
```

# Sequence 192 matched with Sequence 4

```
Query=   Sequence ID - 192                  nt:      286
Length=286


   SEQ ID NO: 4              nt:      286

ALIGNMENTS
 Identities = 286/286 (100%), Gaps = 0/286 (0%)

Query  1    CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTGGGTC  60

Query  61   TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCTGAATTTTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCTGAATTTTA  120

Query  121  GTTAATATACCAATTTCAGTCTCTTGGTTTTGACAGATGTACCATGGTGATGTAAGATGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTAATATACCAATTTCAGTCTCTTGGTTTTGACAGATGTACCATGGTGATGTAAGATGT  180

Query  181  TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTGTACTATCTCTGCAACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTGTACTATCTCTGCAACT  240

Query  241  TCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATTTAATTT    286
            ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATTTAATTT    286
```

# Sequence 250 matched with Sequence 5

```
Query=   Sequence ID 250
Length=545


   SEQ ID NO: 5

ALIGNMENTS
 Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query  1     GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC   60

Query  61    CAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAACTATTGGA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAACTATTGGA   120

Query  121   TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA   180

Query  181   GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG   240

Query  241   CAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT   300

Query  301   CCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGAGATCAGGGACATGTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGAGATCAGGGACATGTT   360

Query  361   GCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC   420

Query  421   TGTGCCAGCCCAGAACACTGGTCTCGGGGCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TGTGCCAGCCCAGAACACTGGTCTCGGGGCCCGAGAAGACCTCCTTTTTCCAGGCTTTAGG   480
```

```
Query  481  TATCACCACTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATCACCACTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
            |||||
Sbjct  541  ACTGG  545
```

## Sequence 299 matched with Sequence 6

Query=  Sequence ID 299
Length=591


   SEQ ID NO: 6

ALIGNMENTS
 Identities = 591/591 (100%), Gaps = 0/591 (0%)

```
Query  1    CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTT  60

Query  61   tttCTCTTTGAAAGATAGAGATTGNTACAACTACTTAAAAAATATAGTCAATAGGTTACT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTCTCTTTGAAAGATAGAGATTGNTACAACTACTTAAAAAATATAGTCAATAGGTTACT  120

Query  121  AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAA  180

Query  181  AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATG  240

Query  241  ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGA  300

Query  301  GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAAT  360

Query  361  GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTG  420

Query  421  AAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGA  480
```

```
Query  481  CGCANGGAGAATTGCGCATTTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGCANGGAGAATTGCGCATTTAAAGCCTAGTTACGCATTTACTAAACGCAGACGAAAATG  540

Query  541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGAAGATTAATTGGGAGTGGTAGGATGAAACAATTTTGGAGAAGATAGAAG  591
```

# Sequence 300 matched with Sequence 7

```
Query=   Sequence ID 300
Length=297


   SEQ ID NO: 7

ALIGNMENTS
 Identities = 297/297 (100%), Gaps = 0/297 (0%)

Query  1    CTCAAAGGAGaaaaaaaaccttgtaaaaaaagcaaaaatgacaacagaaaaaCAATCTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAAAGGAGAAAAAAAACCTTGTAAAAAAAGCAAAAATGACAACAGAAAAACAATCTTA  60

Query  61   TTCCGAGCATTCCAGTAACTTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTCCGAGCATTCCAGTAACTTTTTTGTGTATGTACTTAGCTGTACTATAAGTAGTTGGTT  120

Query  121  TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCttttttttttcctttttttgtct  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCTTTTTTTTTTCCTTTTTTGTCT  180

Query  181  atgaagttgctgtttatttttttttGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCA  240

Query  241  ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTaaaaaaaaaaaaaaaaaaaaaa  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTAAAAAAAAAAAAAAAAAAAAAA  297
```

# Sequence 302 matched with Sequence 8

```
Query=   Sequence ID 302
Length=282


   SEQ ID NO: 8

ALIGNMENTS
 Identities = 282/282 (100%), Gaps = 0/282 (0%)

Query  1    AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATC  60

Query  61   CGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCGCCCAGCCC  120

Query  121  CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTTATTTTGCATA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATTTTATTTTGCATA  180

Query  181  CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAGTTTAGGGCTGGGGGCT  240

Query  241  TATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAATAG   282
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAATAG   282
```

# Sequence 304 matched with Sequence 9

Query=  Sequence ID 304
Length=619


   SEQ ID NO: 9

ALIGNMENTS
 Identities = 619/619 (100%), Gaps = 0/619 (0%)

```
Query  1    TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCtttttgtttttttCAGGGATACCATAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCTTGGTTTCGATTTGTGGCAACAATCCAGTCTTTTTGTTTTTTTCAGGGATACCATAT  60

Query  61   GTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATGTCAAAGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATGTCAAAGTC  120

Query  121  ATCATTTAGTGTAAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATCATTTAGTGTAAACAGCAAGTTATCTGTTAGGCTGCACATCATGAACTTTACTTTTAG  180

Query  181  AAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAGTCATGGATGGCAAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAGTCATGGATGGCAAAGA  240

Query  241  AATTAATTTTGAGTTGTTTGGATAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTAATTTTGAGTTGTTTGGATAAAAATGTTTCAGTTGACTGTAGTGTGTATTGAGAGA  300

Query  301  CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAATCCCCTAGAAGTTACAGAAAATTG  360

Query  361  GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGAGGAGGTGAACTTAATTAAATAACTTGAATTGTTTAGACATATTCAGAGCTTCTTATG  420

Query  421  ACCTTGAAGAAATCACCCAACTTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACCTTGAAGAAATCACCCAACTTCAAAAGACCTCGGTTTCTTCATTTGTAAAATTAGGGA  480
```

```
Query  481  GTTTGACTAGATGTGTAAATCTAGTTGTTAGTTAACTTCTAAGATGTAAAAACCCTCTTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTGACTAGATGTGTAAATCTAGTTGTTAGTTAACTTCTAAGATGTAAAAACCCTCTTG  540

Query  541  TTTAACAAAAACCTACAAGATCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTTAACAAAAACCTACAAGATCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGT  600

Query  601  CACTAAGTCTAGCTCGACC  619
            |||||||||||||||||||
Sbjct  601  CACTAAGTCTAGCTCGACC  619
```

# Sequence 306 matched with Sequence 10

Query=   Sequence ID 306
Length=536


   SEQ ID NO: 10

ALIGNMENTS
 Identities = 536/536 (100%), Gaps = 0/536 (0%)

```
Query  1    CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG  60

Query  61   AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG  120

Query  121  GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA  180

Query  181  ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC  240

Query  241  AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA  300

Query  301  AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA  360

Query  361  TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG  420

Query  421  GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG  480
```

```
Query  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG  536
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCNCATGAANAAATGGACNAGCTGTG  536
```

# Sequence 308 matched with Sequence 11

```
Query=  Sequence ID - 308                nt:     373
Length=373


   SEQ ID NO: 11              nt:     373

ALIGNMENTS
 Identities = 373/373 (100%), Gaps = 0/373 (0%)

Query  1    AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTCAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTTTCAT   60

Query  61   TTTAAAAGTTGGGTCAgtttttttATTAGTACATGTATTTCTATCCTACTGATTTATTTG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGATTTATTTG   120

Query  121  CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGA   180

Query  181  CCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAA   240

Query  241  TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGATATTGCTAAACCAGAAGATA   300

Query  301  ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAANG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNCACATTTAATTAAATTAGAACAANG   360

Query  361  AATGCATAATGNC   373
            |||||||||||||
Sbjct  361  AATGCATAATGNC   373
```

Blast comparison trimmed "NC" from the 3' end of both sequences and reported 371 iden-
tities. The report has been manually corrected for this. "NC" has been appended to both
sequences and identity count has been increased to 373.

# Sequence 309 matched with Sequence 12

Query= Sequence ID 309
Length=796


   SEQ ID NO: 12

ALIGNMENTS
 Identities = 796/796 (100%), Gaps = 0/796 (0%)

```
Query  1    CCGGAATCGCGGCCGCGTCGACGAAAATATGTGCCCTGGCCAACTCCACAGGACTAGTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGGAATCGCGGCCGCGTCGACGAAAATATGTGCCCTGGCCAACTCCACAGGACTAGTTC  60

Query  61   TAGGCAATCTGAAGGAAACCAGAAAATGTGAATTTCTCTTCCCTCAAAAAGCTATACTGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAGGCAATCTGAAGGAAACCAGAAAATGTGAATTTCTCTTCCCTCAAAAAGCTATACTGA  120

Query  121  AGTAGTATTTAATATTCAAGTACTTGTAAATTTGCAGAACAGTACTTTTTAATTTGACCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTAGTATTTAATATTCAAGTACTTGTAAATTTGCAGAACAGTACTTTTTAATTTGACCC  180

Query  181  ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAAACCATCTAAAAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGCAAACCATCTAAAAAGA  240

Query  241  TTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCACATAttttttaactttttCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCACATATTTTTTAACTTTTTCT  300

Query  301  AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACAACACAAAGGGATATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATTTGAAAAGTAATACAGGCATATGGTATTTTAAAAATGAAACAACACAAAGGGATATG  360

Query  361  TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTTGAAAAGTGGTCTTGCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGT  420

Query  421  TTTCATTTTAAAAGTTGGGTCAGttttttttATTAGTACATGTATTTCTATCCTACTGATT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTTTAAAAGTTGGGTCAGTTTTTTTTATTAGTACATGTATTTCTATCCTACTGATT  480
```

```
Query  481  TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTA  540

Query  541  TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTG  600

Query  601  NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  NATAAATCCTACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCA  660

Query  661  GAAGATAACCTGCATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GAAGATAACCTGCATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTA  720

Query  721  GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  GAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAA  780

Query  781  GGAAAGCAAAACTGTC  796
            ||||||||||||||||
Sbjct  781  GGAAAGCAAAACTGTC  796
```

## Sequence 310 matched with Sequence 13

```
Query=   Sequence ID - 310 nt:564
Length=564


   SEQ ID NO: 13                   nt:564

ALIGNMENTS
 Identities = 564/564 (100%), Gaps = 0/564 (0%)

Query  1    CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANGATTT  60

Query  61   AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTGTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTATTTTTTGTG  120

Query  121  TGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCCACCTATATCTAN  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCCACCTATATCTAN  180

Query  181  CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGAGTANTATAGAAGCTGT  240

Query  241  CAATATGTATCTACTGTACAGTACTAAATAGTATTCATTTATGAAATGAGTAGTGTTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAATATGTATCTACTGTACAGTACTAAATAGTATTCATTTATGAAATGAGTAGTGTTTGG  300

Query  301  GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTTGAGTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTGTAGCTTTTATCCAAGTTTTGAGTA  360

Query  361  TAAATAGGGttttgttttgttttttttAACCTAAAAACTGAAATGCCATATAGAAAAACA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAAATAGGGTTTTGTTTTGTTTTTTTTAACCTAAAAACTGAAATGCCATATAGAAAAACA  420

Query  421  GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTAAAGATTTTATCAAAAAGAATTTTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCATTGTTTTTACAGTTTGTAGTAAGTAACTTTTTAAAGATTTTATCAAAAAGAATTTTG  480
```

```
Query  481   TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTTAAAAAACAAA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TCTATNGTGAGTAAAAGAAGTTCTAATAATGGCCTAATCACTGCATTTTTAAAAAACAAA   540

Query  541   GTTCAACACAAATGACATTTGTTT   564
             ||||||||||||||||||||||||
Sbjct  541   GTTCAACACAAATGACATTTGTTT   564
```

# Sequence 311 matched with Sequence 14

```
Query=  Sequence ID 311
Length=230


   SEQ ID NO: 14

ALIGNMENTS
 Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query  1    CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTAAGCA  60

Query  61   ACAGCCCCAAATGCTGGCTGCCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAGCCCCAAATGCTGGCTGCCCCCGGCCAAGCATTGGGGCCGCCATCCTGCCTGGCACT  120

Query  121  GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAGGCCCCGCAGTCC  180

Query  181  CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG  230
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTCCATTGG  230
```

# Sequence 313 matched with Sequence 15

```
Query=  Sequence ID - 313                    nt:     554
Length=554


   SEQ ID NO: 15              nt:     554

ALIGNMENTS
 Identities = 554/554 (100%), Gaps = 0/554 (0%)

Query    1  CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC  60

Query   61  TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA  120

Query  121  AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA  180
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||
Sbjct  121  AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA  180

Query  181  TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT  240

Query  241  CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG  300

Query  301  GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA  360

Query  361  TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG  420

Query  421  GAGCGATAACCCGGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGCGATAACCCGGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG  480
```

```
Query  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540

Query  541  GAACTATTATATGC  554
            ||||||||||||||
Sbjct  541  GAACTATTATATGC  554
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 314 matched with Sequence 16

Query=   Sequence ID 314
Length=610


   SEQ ID NO: 16

ALIGNMENTS
 Identities = 610/610 (100%), Gaps = 0/610 (0%)

```
Query  1    CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG  60

Query  61   AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG  120

Query  121  GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA  180

Query  181  ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC  240

Query  241  AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA  300

Query  301  AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA  360

Query  361  TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG  420

Query  421  GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG  480
```

```
Query  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540

Query  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCAC  600

Query  601  AATCATGAGG  610
            ||||||||||
Sbjct  601  AATCATGAGG  610
```

# Sequence 315 matched with Sequence 17

```
Query=   Sequence ID 315
Length=359


   SEQ ID NO: 17

ALIGNMENTS
 Identities = 359/359 (100%), Gaps = 0/359 (0%)

Query  1    TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGCCCCT  60

Query  61   CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGCCATAATCC  120

Query  121  ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCCCTGAAACA  180

Query  181  GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAGGGGTTGATGCCAGACA  240

Query  241  TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGCAACAGCCAAAATAGGGGGGT  300

Query  301  AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTACTTG  359
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGTCAATAAAGTTACCCTTGTACTTG  359
```

# Sequence 316 matched with Sequence 18

```
Query=   Sequence ID 316
Length=154


   SEQ ID NO: 18

ALIGNMENTS
 Identities = 154/154 (100%), Gaps = 0/154 (0%)

Query  1    CGCCACTTATCCAGTGAACCACTATCACGaaaaaaaaCTCTACCTCTCTATACTAATCTCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGCCACTTATCCAGTGAACCACTATCACGAAAAAAAACTCTACCTCTCTATACTAATCTCC  60

Query  61   CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTaaaaaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAAAAAAAAAA  120

Query  121  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa   154
            ||||||||||||||||||||||||||||||||||
Sbjct  121  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   154
```

# Sequence 321 matched with Sequence 19

Query=  Sequence ID 321
Length=661


   SEQ ID NO: 19

ALIGNMENTS
 Identities = 661/661 (100%), Gaps = 0/661 (0%)

```
Query  1    CAGAACAGTACTTTTTAATTTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAACAGTACTTTTTAATTTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTA  60

Query  61   GCCAAGAAGCAAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACTCCTAATAAATAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCCAAGAAGCAAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACTCCTAATAAATAG  120

Query  121  GGTCACATAtttttaacttttttCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTCACATATTTTTTAACTTTTTTCTAATTTGAAAAGTAATACAGGCATATGGTATTTTA  180

Query  181  AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTTGCCATCCCTGAACTGT  240

Query  241  AATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGttttttttATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGTTTTTTTATT  300

Query  301  AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAGTTTGAATAT  360

Query  361  TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTA  420

Query  421  TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAACAATGCTACAGTGAATATTGGTGTATAAATCCATACACACCACGTAACATATCTTA  480
```

```
Query  481  AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTTAAAATTTTGACTGCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTGCATTTAAAATTTTGACTGCT  540

Query  541  AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCA  600

Query  601  ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAAACTGTCAATAACTTTCTTCTC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ATCTATTCCAGGTGCACCGTGGTCACAAAGGAAAGCAAAACTGTCAATAACTTTCTTCTC  660

Query  661  A  661
            |
Sbjct  661  A  661
```

# Sequence 322 matched with Sequence 20

```
Query=   Sequence ID 322
Length=770


   SEQ ID NO: 20

ALIGNMENTS
 Identities = 770/770 (100%), Gaps = 0/770 (0%)

Query  1    TAGCATTTGGCCTTTTAAAACATTTGTTTAtttttttttCTGAGAATGGCTAACACACTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAGCATTTGGCCTTTTAAAACATTTGTTTATTTTTTTTTCTGAGAATGGCTAACACACTTT  60

Query  61   ATTGAGGTTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATTCTGTATGT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTGAGGTTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATTCTGTATGT  120

Query  121  TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTTTGTCTTGGAGAA  180

Query  181  GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACTAGAGAATGAGAAG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACAACTAGAGAATGAGAAG  240

Query  241  AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTAGCACGTCATCTGCTACTGAG  300

Query  301  TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAATTAAGGA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATGGTGTGATAACATTGTGTAACAGGAAAGTATGATCAATATCTACTTAAAATTAAGGA  360

Query  361  CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAATATTAGCACTACATTGCTTTATTTTAAAGTAAAAATTAGAGAACTAAACACAAGCAT  420

Query  421  TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTAAGTACAATAAAAGCTGATCTTTCTAGTTAAGCAGAATAATACATGTTCAAGCATCT  480
```

```
Query  481  GCTAAATCATTAAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCTAAATCATTAAATATAAGAATATAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAG  540

Query  541  TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TACCTCATTTTCAAGANGAGAAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTT  600

Query  601  TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTAATGTTCCCAGCACAAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGA  660

Query  661  ATCCCTTGTCATACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  ATCCCTTGTCATACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTT  720

Query  721  ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT    770
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  ATAATCTTTTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT    770
```

# Sequence 323 matched with Sequence 21

```
Query=   Sequence ID 323
Length=654
```

```
   SEQ ID NO: 21
```

```
ALIGNMENTS
 Identities = 654/654 (100%), Gaps = 0/654 (0%)
```

```
Query  1    CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGA   60

Query  61   AAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACC   120

Query  121  AGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAAT   180

Query  181  GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAG   240

Query  241  TGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGG   300

Query  301  AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTGAA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAAGATTAACCAGTGTGAA   360

Query  361  CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAGAA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAGAA   420

Query  421  TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGA   480
```

```
Query  481  ATGGACTGGCGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGGACTGGCGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAA  540

Query  541  CTGACCTGCTATCCCACCCCAAATTCAACCTGAGGTATATTTCAGTGAAGCAGGTAGCTG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTGACCTGCTATCCCACCCCAAATTCAACCTGAGGTATATTTCAGTGAAGCAGGTAGCTG  600

Query  601  TGCTTCTCAAAGCAGAGAAGCAGTTTTAAGAACCAAAAAGGTAGAGGAAATCTA   654
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGCTTCTCAAAGCAGAGAAGCAGTTTTAAGAACCAAAAAGGTAGAGGAAATCTA   654
```

# Sequence 324 matched with Sequence 22

Query=   Sequence ID 324
Length=676


   SEQ ID NO: 22

ALIGNMENTS
 Identities = 676/676 (100%), Gaps = 0/676 (0%)

```
Query  1    GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGaa  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCCTGAA  60

Query  61   aaaaaTTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAATTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAACAAAATGT  120

Query  121  AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAGCATATCTGCCTT  180

Query  181  TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTAttttttttAAAA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  181  TTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGCCTGTATTTTTTTAAAA  240

Query  241  TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATAGTTAAACTTCACCCTCTTTA  300

Query  301  ATTTCACAACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTTCACAACATATTCTTTGGAAGCAGGAAGAAATGCTCATAAAGAGGATCAGACCTTCT  360

Query  361  TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCCCGTGAAACCAGTATTTGGCGCCATATATAAGCCTGGTTAAATTGGTCATCTAAAGC  420

Query  421  TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTCAAATAAGACATTCTGTGAAAGGTAAACATCGAAACTGGTTATAAGTAAAACCATCA  480
```

```
Query  481  AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCCAACAACAGGGTCTTGAGATAACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGA  540

Query  541  TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGTCTGCATTACTCATTGCTAAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTC  600

Query  601  AAGAAGAAATTTAAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAGAAGAAATTTAAACTTACGTTTGGGTTTCCATACAGCACTCTATTGAATACATGCATC  660

Query  661  TGAATTTAAGTTGCAA    676
            ||||||||||||||||
Sbjct  661  TGAATTTAAGTTGCAA    676
```

## Sequence 325 matched with Sequence 23

```
Query=   Sequence ID 325
Length=609


   SEQ ID NO: 23

ALIGNMENTS
 Identities = 609/609 (100%), Gaps = 0/609 (0%)

Query  1    GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCATTGTCTCCCTAGTTAATTACAGGTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCATTGTCTCCCTAGTTAATTACAGGTGG  60

Query  61   GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTTTGTGGAAC  120

Query  121  TCCTTAAAGTTGTAGCTGTCATGATCAGAtttttttttATATTTCCTCAGCTTAACTCTGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCTTAAAGTTGTAGCTGTCATGATCAGATTTTTTTTTATATTTCCTCAGCTTAACTCTGC  180

Query  181  TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TACTTGATTTACAGTGACCCATAACCTACTCATCCTTGGTTTATAGTGACACATAATCTT  240

Query  241  ATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCTTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCTTAGAATACAGCATTTCTTTG  300

Query  301  CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGTAACTCTGATCAATCAATTATCCAT  360

Query  361  AAGGAAGGGCTTTTCATGGGTTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAGGAAGGGCTTTTCATGGGTTCTATTAATTTGTTAGTACCCTAAGTATATCTGAAAAAT  420

Query  421  ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATGTCTATTGAGAGAAGATTTTGGCATTCCAGATGGTATAGTCTATATATATTTAAAGTT  480
```

```
Query  481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTTCTAGCATTTTTGCATTTACCTGTTAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGAATTTGCTTATATATACTCAGCTTTCTTTTTCTAGCATTTTTGCATTTACCTGTTAA  540

Query  541  TTGAAGTATACCCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGAAGTATACCCCCCACATATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGG  600

Query  601  GCTAAAATA  609
            |||||||||
Sbjct  601  GCTAAAATA  609
```

# Sequence 326 matched with Sequence 24

```
Query=   Sequence ID - 326              nt:     554
Length=554


   SEQ ID NO: 24            nt:     554

ALIGNMENTS
 Identities = 554/554 (100%), Gaps = 0/554 (6%)

Query    1  CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAGGAAC   60

Query   61  TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  TTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTTATAGATTA  120

Query  121  AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA  180
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||| |||
Sbjct  121  AAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGATATGGATTANAAA  180

Query  181  TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAATATGGATTAAAAAACAT  240

Query  241  CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGG  300

Query  301  GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTTTTTAATATGGATTAAACATCTGTGGGTTTTTAATATGGGTTAAAAATCAAAAGAAAA  360

Query  361  TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAACTATTTGCTCCAGTGCAGGAAAATACAGGCAATACTGGATACAATTAGATGGTCAG  420

Query  421  GAGCGATAACCCGGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGCGATAACCCGGTTGCCATTGTTTGAAGAAGAGAATAAGGNGCTAGCATTCCTATCCG  480
```

```
Query  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAGATAATTTGACAGCTAGGAAATAGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAAT  540

Query  541  GAACTATTATATGC  554
            ||||||||||||||
Sbjct  541  GAACTATTATATGC  554
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 327 matched with Sequence 25

Query=  Sequence ID 327
Length=674


   SEQ ID NO: 25

ALIGNMENTS
 Identities = 674/674 (100%), Gaps = 0/674 (0%)

```
Query  1     CGGCTACCGACAGAAGGACTATTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CGGCTACCGACAGAAGGACTATTTCATCGCCACCCAGGGGCCACTGGCACACACGGTTGA   60

Query  61    GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTGACGGAGGT   120

Query  121   GCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGGCTCAGTTACTCA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGGCTCAGTTACTCA   180

Query  181   TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAGCCATCAGTATACGAGA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAGCCATCAGTATACGAGA   240

Query  241   CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAGGAGCAGGTCCGAGTAGTGCG   300

Query  301   CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGATTCCCGCCGAGGGCAAAGGCATGAT   360

Query  361   TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TGACCTCATCGCAGCCGTGCAGAAGCANCAGCAGCAGACAGGCAACCACCCCATCACCGT   420

Query  421   GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GCACTGCAGTGCCGGAGCTGGGCGAACAGGTACATTCATAGCCCTCAGCAACATTTTGGA   480
```

```
Query  481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCGAGTAAAAGCCGAGGGACTTTTANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCA  540

Query  541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAGACCACATATGGTGCAACCCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGAT  600

Query  601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTATTGATATATTTCTGATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTA  660

Query  661  ATTTAATGGCANAT    674
            |||||||||||||
Sbjct  661  ATTTAATGGCANAT    674
```

Blast comparison trimmed "NAT" from the 3' end of both sequences and reported 671 identities. The report has been manually corrected for this. "NAT" has been appended to both sequences and identity count has been increased to 674.

# Sequence 328 matched with Sequence 26

Query=  Sequence ID 328
Length=609


   SEQ ID NO: 26


ALIGNMENTS
 Identities = 609/609 (100%), Gaps = 0/609 (0%)

```
Query  1    CAAGACTCCATCTCaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC  60

Query  61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT  120

Query  121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT  180

Query  181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT  240

Query  241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT  300

Query  301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT  360

Query  361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA  420

Query  421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA  480
```

```
Query  481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTANAAGCATTCCTGCGTAA   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTANAAGCATTCCTGCGTAA   540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA   600

Query  601  GTGGTTTTT  609
            |||||||||
Sbjct  601  GTGGTTTTT  609
```

# Sequence 330 matched with Sequence 27

Query= Sequence ID 330
Length=383


    SEQ ID NO: 27

ALIGNMENTS
 Identities = 383/383 (100%), Gaps = 0/383 (0%)

```
Query  1    GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGaaaaaaaaccttgtaaaaaaagcaaa  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGAAAAAAAACCTTGTAAAAAAAGCAAA  60

Query  61   aatgacaacagaaaaaCAATCTTATTCCGAGCATTCCAGTAACTTTTTTGTGTATGTACT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAACTTTTTTGTGTATGTACT  120

Query  121  TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGT  180

Query  181  TTCtttttttttcctttttgtctatgaagttgctgtttattttttttGGCCTGTTTGAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTCTTTTTTTTTCCTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGAT  240

Query  241  GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCT  300

Query  301  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaatttaaatt  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAAAATT  360

Query  361  tttaaaataaaaCCCTTGGTTAT  383
            |||||||||||||||||||||||
Sbjct  361  TTTAAAATAAAACCCTTGGTTAT  383
```

# Sequence 331 matched with Sequence 28

Query=   Sequence ID 331
Length=729


   SEQ ID NO: 28

ALIGNMENTS
 Identities = 729/729 (100%), Gaps = 0/729 (0%)

```
Query  1    GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTGGTTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTGGTTG  60

Query  61   AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTTCTGAGGTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTTCTGAGGTG  120

Query  121  GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAGTTGAACAAAGCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAGTTGAACAAAGCA  180

Query  181  GCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAATAATCAGGCTTTTTAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAATAATCAGGCTTTTTAAA  240

Query  241  TGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAGCAGCTGCTGGTGGCTTGGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAGCAGCTGCTGGTGGCTTGGGA  300

Query  301  CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTC  360

Query  361  TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGTGGGAAGAGGGCCATCTGCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGTGGGAAGAGGGCCATCTGCC  420

Query  421  TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGGCTTGTGTGAGCGTGTGGAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGGCTTGTGTGAGCGTGTGGAC  480
```

```
Query  481   AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCT   540

Query  541   GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GCTTCAACCTGCACCCCTCCTTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAAT   600

Query  601   ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ATGGATGGGAAAGCTCCTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGT   660

Query  661   CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCAC   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CTGCCTGGGTGTGGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCAC   720

Query  721   TTGGGCCCC   729
             |||||||||
Sbjct  721   TTGGGCCCC   729
```

# Sequence 335 matched with Sequence 29

Query=   Sequence ID 335
Length=552


    SEQ ID NO: 29

ALIGNMENTS
 Identities = 552/552 (100%), Gaps = 0/552 (0%)

```
Query   1    CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAA   60

Query   61   GAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTA   120

Query   121  CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGA   180

Query   181  ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCC   240

Query   241  AGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCT   300

Query   301  GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAAAGATTAACCAGTGTG   360

Query   361  AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAG   420

Query   421  AATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAA   480
```

```
Query   481   GAATGGACTGGCGGCGTGGGTGAGCTGATTTGGAAAACTGCCCTTCTGCAAAAAACACTG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GAATGGACTGGCGGCGTGGGTGAGCTGATTTGGAAAACTGCCCTTCTGCAAAAAACACTG   540

Query   541   GCCTGCTTTCCA   552
              ||||||||||||
Sbjct   541   GCCTGCTTTCCA   552
```

# Sequence 337 matched with Sequence 30

Query=   Sequence ID 337
Length=606


   SEQ ID NO: 30

ALIGNMENTS
 Identities = 606/606 (100%), Gaps = 0/606 (0%)

```
Query   1    CAAGACTCCATCTCaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC   60

Query   61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT   120

Query   121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT   180

Query   181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT   240

Query   241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT   300

Query   301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT   360

Query   361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA   420

Query   421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA   480
```

```
Query  481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAA  540

Query  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query  601  GTGGTT  606
            ||||||
Sbjct  601  GTGGTT  606
```

# Sequence 338 matched with Sequence 31

```
Query=   Sequence ID 338
Length=734


   SEQ ID NO: 31

ALIGNMENTS
 Identities = 734/734 (100%), Gaps = 0/734 (0%)

Query  1    CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAAAGAG  60

Query  61   GATACCATATGTGGGTGCCggggggggATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG  120
            ||||||||||||||||||||||||         |||||||||||||||||||||||||||
Sbjct  61   GATACCATATGTGGGTGCCGGGGGGGGGATAGGTGAGAAGTACTAGAAGGCGGAATGGAAGG  120

Query  121  ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCAGGTCCTTTAACA  180

Query  181  CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACAAGTATGCAGACTAAGC  240

Query  241  TCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAACATGCATATATGTTCTCATTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAACATGCATATATGTTCTCATTC  300

Query  301  ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGGTACATGAACTCAGAAGCCTTACTGCCTATTTTTGTTAATACTTCTGGGCAAACATT  360

Query  361  ACCACTTACAACTCACACCAGTTAGAAATCATTTGTAAAATGTTATTTAATAAAGCCAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACCACTTACAACTCACACCAGTTAGAAATCATTTGTAAAATGTTATTTAATAAAGCCAAA  420

Query  421  GAACTAAATCATATTTATTTTCCAAGGNTTTCTAAGATCTCTGAAACTAATGAGGTTTTT  480
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  421  GAACTAAATCATATTTATTTTCCAAGGNTTTCTAAGATCTCTGAAACTAATGAGGTTTTT  480
```

```
Query  481  TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAATCCCCATTAAGTACTCATCACTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCC  540

Query  541  AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGTGAGTCCCCTTAAATTTATTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGT  600

Query  601  GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGTCACCCTAATTTAANGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCT  660

Query  661  AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTNATCCTTTCCC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  AANCCTTGAATAATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTNATCCTTTCCC  720

Query  721  TTTTTTATCCCATG   734
            ||||||||||||||
Sbjct  721  TTTTTTATCCCATG   734
```

# Sequence 339 matched with Sequence 32

Query= Sequence ID 339
Length=517


    SEQ ID NO: 32

ALIGNMENTS
 Identities = 517/517 (100%), Gaps = 0/517 (0%)

```
Query  1    ttttttttAAATAAAGCTGTCGGCACTCAAGGGTAATTTCATATCAGTGTGNTCTACAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTAAATAAAGCTGTCGGCACTCAAGGGTAATTTCATATCAGTGTGNTCTACAA  60

Query  61   GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTAGCATAAAG  120

Query  121  GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCACCCCTTTTTCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACCACCCCTTTTTCT  180

Query  181  GTCTGAAAAAACAACTAAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTCTGAAAAAACAACTAAAACAATATTACAACAGTATAGTTACAGAAGGGTTCTATTTTC  240

Query  241  ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAAATATATATACTTTTGAGGGG  300

Query  301  GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCCATTTCTAGGTGTGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGATACAACCCCATTTCTAGGTGTGAG  360

Query  361  GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTCTAAATGCTTCACACACCCACTTGTGACCTTTTTTCATGAAGAATCATAACACTGTGC  420

Query  421  AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTTAAAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTGAGAAACAGTGGCAAAGCAATACTGAAAGCATTTTAAATTATTTACTAGGTTAAAAG  480
```

```
Query  481  GGTGAACTGATACTTTAAATACATCAAATTTCATCAT  517
            |||||||||||||||||||||||||||||||||||||
Sbjct  481  GGTGAACTGATACTTTAAATACATCAAATTTCATCAT  517
```

# Sequence 360 matched with Sequence 33

Query=   Sequence ID 360
Length=536


   SEQ ID NO: 33

ALIGNMENTS
 Identities = 536/536 (100%), Gaps = 0/536 (0%)

Query  1     GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAACTAA   60

Query  61    ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTTTTTG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTTTTTG   120

Query  121   TGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAGTCAACTTCTCAG   180

Query  181   AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAAT   240

Query  241   TTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATCC   300

Query  301   CTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATCCCAATGCACCCAAGAGGCCTCCTT   360

Query  361   CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCCAAAAATCAAAGGAGAACATCCTGGCC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CGGCCTTCTTCCTCTTCTGCTCTGAGTATCGCCCAAAAATCAAAGGAGAACATCCTGGCC   420

Query  421   TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATG   480

```
Query  481  ACAAGCAGCCTTATGAAAAGAAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGTA  536
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACAAGCAGCCTTATGAAAAGAAGGCTGCGAAGCTGAAGGAAAAATACGAAAAGGTA  536
```

# Sequence 361 matched with Sequence 34

```
Query=   Sequence ID - 361                    nt:       622
Length=622


   SEQ ID NO: 34            nt:       622

ALIGNMENTS
 Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query  1     CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAGGTGC  60

Query  61    ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTGGAATTTGT  120

Query  121   ACCATGATCAGTGTGAATCCCANTGGCGTAATCCAAGTAAGATGTTCACAAAGATTTGTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACCATGATCAGTGTGAATCCCANTGGCGTAATCCAAGTAAGATGTTCACAAAGATTTGTT  180

Query  181   TTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAA  240

Query  241   AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAA  300

Query  301   TATCTTGAAATTGTAATGCCttttttttttcctaaattttttttGTCATGAAATGAGATA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAATTTTTTTTGTCATGAAATGAGATA  360

Query  361   GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTT  420

Query  421   TCATCCAAATTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCATCCAAATTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCA  480
```

```
Query  481  NGTTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  NGTTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATT  540

Query  541  CTGAATAAAATACTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCACCATTGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTGAATAAAATACTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCACCATTGA  600

Query  601  AATTGCTCTAATTTTGAGAGCT  622
            ||||||||||||||||||||||
Sbjct  601  AATTGCTCTAATTTTGAGAGCT  622
```

# Sequence 363 matched with Sequence 35

```
Query=  Sequence ID - 363                nt:     628
Length=628


   SEQ ID NO: 35           nt:     628

ALIGNMENTS
 Identities = 628/628 (100%), Gaps = 0/628 (0%)

Query  1    ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCTACAA  60

Query  61   AAATATAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCCAGCTACTCGGGAGGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAATATAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCCAGCTACTCGGGAGGCT  120

Query  121  GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCA  180

Query  181  CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataataa  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAATAATAATAATAA  240

Query  241  taataataaaaaggaataacatagctaggaataaatttaatCAAAGAGGTGAAAGACTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAATAATAAAAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTA  300

Query  301  TACACTTAAAACTACaaaaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaataaa  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACACTTAAAACTACAAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAA  360

Query  361  taaaaaGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAAAAAGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTA  420

Query  421  CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTA  480
```

```
Query  481  GAAATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAA  540

Query  541  ACAATCTTGGGGaaaaaaaacaaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACAATCTTGGGGAAAAAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATA  600

Query  601  AATTTACTACAAAGTTATAGTAATCAAA  628
            ||||||||||||||||||||||||||||
Sbjct  601  AATTTACTACAAAGTTATAGTAATCAAA  628
```

# Sequence 364 matched with Sequence 36

```
Query=  Sequence ID - 364                  nt:     528
Length=527


   SEQ ID NO: 36             nt:     528

ALIGNMENTS
 Identities = 527/527 (100%), Gaps = 0/527 (0%)

Query  1    TGAACATCCAGCCATGTCATTTCTTCCATTCCTGCCCTGGAGTAAAGTAGATTTACTGAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGAACATCCAGCCATGTCATTTCTTCCATTCCTGCCCTGGAGTAAAGTAGATTTACTGAG  60

Query  61   CTGATGACTTGTGTGCATTTGTACATTGCAACCTTAGCTTACCTCTTGAAGCATGTAGAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGATGACTTGTGTGCATTTGTACATTGCAACCTTAGCTTACCTCTTGAAGCATGTAGAG  120

Query  121  CATTCATCACCCACCATTCATTCACTGCCTACTCCCACCACAGCTGTTTCGTGGTCTGTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATTCATCACCCACCATTCATTCACTGCCTACTCCCACCACAGCTGTTTCGTGGTCTGTC  180

Query  181  TGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAAGTGATGAAGTCACCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAAGTGATGAAGTCACCTG  240

Query  241  TGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGGCCTCTTCCTCTTGCTCAAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGGCCTCTTCCTCTTGCTCAAGA  300

Query  301  GGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGCCTCCATCCCAGTTCACCTTTTCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGCCTCCATCCCAGTTCACCTTTTCAG  360

Query  361  AAATGGCCCCTCAGTCAACTCTTCCCTTTTCTCCTGGCTTTTTATTTCTCCCAGTCTCTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAATGGCCCCTCAGTCAACTCTTCCCTTTTCTCCTGGCTTTTTATTTCTCCCAGTCTCTT  420

Query  421  AAGAGTATCCTTAGCTTTAAAAACAATAACACAGAGGATGGGTGCAGTGGCTCATGCCTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGAGTATCCTTAGCTTTAAAAACAATAACACAGAGGATGGGTGCAGTGGCTCATGCCTG  480
```

```
Query  481  TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGGNCA  527
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAATCCCAGCACTTTGGAGCCTGGGGCGGGCGGATCACTTGAGGNCA  527
```

Blast comparison trimmed "NCA" from the 3' end of both sequences and reported 524 identities. The report has been manually corrected for this. "NCA" has been appended to both sequences and identity count has been increased to 527.

# Sequence 365 matched with Sequence 37

```
Query=   Sequence ID 365
Length=403


   SEQ ID NO: 37

ALIGNMENTS
 Identities = 403/403 (100%), Gaps = 0/403 (0%)

Query  1    GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCTTGCA  60

Query  61   AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGACAGCTTTGT  120

Query  121  ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGCCCTAAAATACCA  180

Query  181  ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGAACCAGCACTTCTGCTG  240

Query  241  AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCCAGACCCCAGTGGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCCATGCCCAGACCCCAGTGGCT  300

Query  301  CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGCTGTTGCAACCTGGGCATGAGGAGG  360

Query  361  AGTGCAAGATGGCTTTGTCCTACCTGGAAAGAGGCTTTCTGGA  403
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTGCAAGATGGCTTTGTCCTACCTGGAAAGAGGCTTTCTGGA  403
```

# Sequence 366 matched with Sequence 38

```
Query=   Sequence ID 366
Length=111


   SEQ ID NO: 38

ALIGNMENTS
 Identities = 111/111 (100%), Gaps = 0/111 (0%)

Query  1    CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTGTTAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTGTTAT   60

Query  61   AACATTGAGaaaaaaaTTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT   111
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACATTGAGAAAAAAATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT   111
```

# Sequence 368 matched with Sequence 39

```
Query=  Sequence ID - 368                    nt:     329
Length=329


   SEQ ID NO: 39              nt:     329

ALIGNMENTS
 Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA  60

Query  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG  120

Query  121  AGACACAAAAAACCATTCaaaaaaaaaCAATGAATCCAGGAGttttttttttAAAAAGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT  180

Query  181  CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT  240

Query  241  CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAAACTACCATCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAAACTACCATCA  300

Query  301  GAGAACACTATAAACACCTCTATGCAAAT    329
            |||||||||||||||||||||||||||||
Sbjct  301  GAGAACACTATAAACACCTCTATGCAAAT    329
```

# Sequence 369 matched with Sequence 40

```
Query=   Sequence ID 369
Length=341


   SEQ ID NO: 40

ALIGNMENTS
 Identities = 341/341 (100%), Gaps = 0/341 (0%)

Query  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA   60

Query  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG   120

Query  121  AGACACAAAAAACCATTCaaaaaaaaaCAATGAATCCAGGAGtttttttttttAAAAAGAT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTTAAAAAGAT   180

Query  181  CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAGAAGCATCAAATAGACT   240

Query  241  CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAAACTACCATCA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAATAAAAAATGATAAAGGGGATATCACCACCAATCCCACAGAAATACAAACTACCATCA   300

Query  301  GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT   341
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGAACACTATAAACACCTCTATGCAAATAAACTAGAAAAT   341
```

# Sequence 370 matched with Sequence 41

```
Query=   Sequence ID 370
Length=185


   SEQ ID NO: 41

ALIGNMENTS
 Identities = 185/185 (100%), Gaps = 0/185 (0%)

Query  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGAGCAA  60

Query  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAAAGAGATAG  120

Query  121  AGACACAAAAAACCATTCaaaaaaaaaCAATGAATCCAGGAGttttttttttAAAAAGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTTTTTTAAAAAGAT  180

Query  181  CAACA  185
            |||||
Sbjct  181  CAACA  185
```

# Sequence 371 matched with Sequence 42

```
Query=   Sequence ID 371
Length=553


   SEQ ID NO: 42

ALIGNMENTS
 Identities = 553/553 (100%), Gaps = 0/553 (0%)

Query  1    GCCCGGAATCGCGGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCCGGAATCGCGGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACAGGAA  60

Query  61   AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCCTCAGNT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTCCCTCAGNT  120

Query  121  NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTTAATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  NCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTTTCCTTTTTAATG  180

Query  181  GCCAGGTACAGCTGCTTATATGGANGGGCATTTNTNAATGATATCCTTNATCACTGTCTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCAGGTACAGCTGCTTATATGGANGGGCATTTNTNAATGATATCCTTNATCACTGTCTT  240

Query  241  AATCATCACATNCTTAAAACAATCACTTTATTGTGTTAAGGAAGATAAAAATGGCTGGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATCATCACATNCTTAAAACAATCACTTTATTGTGTTAAGGAAGATAAAAATGGCTGGGT  300

Query  301  TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGTAACCATTTAATAATGCANAGGGCA  360

Query  361  NTTTCACTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAAACTTCTACTTTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  NTTTCACTGCAGACCCTAATACTGGAAATTTTTAAAAACAAATGAAAAACTTCTACTTTT  420

Query  421  TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAACT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TCTTCTAAGCTTACTTAACCACCCAAATTTTCCAGCCACATATCTTCCTAGTCTACAACT  480
```

```
Query  481  GCCTTTAACTTTAAGAGATGCTCaaaaaaaTGTAAATTCTCAAATACATTCTTATTACAA   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCCTTTAACTTTAAGAGATGCTCAAAAAAATGTAAATTCTCAAATACATTCTTATTACAA   540

Query  541  TTACTGCTAACCT   553
            |||||||||||||
Sbjct  541  TTACTGCTAACCT   553
```

# Sequence 373 matched with Sequence 43

```
Query=  Sequence ID 373
Length=510


   SEQ ID NO: 43

ALIGNMENTS
 Identities = 510/510 (100%), Gaps = 0/510 (0%)

Query  1    CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCATATGA  60

Query  61   TATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGTCTGGAGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGTCTGGAGAT  120

Query  121  ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAGAGGTCAGGGATG  180

Query  181  GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAGCCCCAAATGTCAGTAG  240

Query  241  GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAGGACAGACTGGCCTGGAAGTG  300

Query  301  TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTAAGGCCAAAGGAAAAAAGGAATGCA  360

Query  361  GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAACCCTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGAAATGCCCGTTAAAAATCTTCAAAACAATATAAAATGATCAATTCCACTAAAACCCTT  420

Query  421  TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACACATTTAAGTATAAAGGTATTGGTAGGAAAATTTGTTATTCACTGCTTTTCTCAGTG  480
```

```
Query  481  TCATGAAATAATTATTTCTGCTGTCAGTTT  510
            ||||||||||||||||||||||||||||||
Sbjct  481  TCATGAAATAATTATTTCTGCTGTCAGTTT  510
```

# Sequence 374 matched with Sequence 44

```
Query=   Sequence ID 374
Length=335


   SEQ ID NO: 44

ALIGNMENTS
 Identities = 335/335 (100%), Gaps = 0/335 (0%)

Query  1    aaaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaataaataaaaaGACATTCTG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAGACATTCTG  60

Query  61   TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTAC  120

Query  121  AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCA  180

Query  181  ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGaaa  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGAAA  240

Query  241  aaaaacaaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTT  300

Query  301  ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG  335
            |||||||||||||||||||||||||||||||||||
Sbjct  301  ATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG  335
```

# Sequence 378 matched with Sequence 45

```
Query=   Sequence ID 378
Length=314


   SEQ ID NO: 45

ALIGNMENTS
 Identities = 314/314 (100%), Gaps = 0/314 (0%)

Query  1    CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGCGGCGGTCGGAGAAGTGGCCTAAAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGCGGCGGTCGGAGAAGTGGCCTAAAA   60

Query  61   CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAGTCCACCGG   120

Query  121  TGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAGCGCTCCCTCTAC   180

Query  181  CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGGCGCTTCGAGAGATTCG   240

Query  241  TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTGCCCTTCCAGAGGTTGGTGAG   300

Query  301  GGANATCGCCCAGG   314
            |||||||||||||||
Sbjct  301  GGANATCGCCCAGG   314
```

# Sequence 380 matched with Sequence 46

Query= Sequence ID 380
Length=537


   SEQ ID NO: 46

ALIGNMENTS
 Identities = 537/537 (100%), Gaps = 0/537 (0%)

```
Query  1    GCAATTTAATTTTTAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCAATTTAATTTTTAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTGGCTA  60

Query  61   AGTCCAGATTaaaaaaaaaaaGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGTCCAGATTAAAAAAAAAAAGTATCTAGCCCAACAGTACAATTATACAGCTTTGTACAG  120

Query  121  AACATTCCATAGATCAACAGAAAATACATTTGAGCGCaaaaataaaaaaTATTTAAGGAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AACATTCCATAGATCAACAGAAAATACATTTGAGCGCAAAAATAAAAAATATTTAAGGAG  180

Query  181  AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTCTGATTAAATATCTACA  240

Query  241  AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGACTAAGTCATTAACAATGACCT  300

Query  301  GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGTAATTCTTTCACTTCAATTTGAATGATTTATAAGCTAAATCTTCAACCACAAAAAGGT  360

Query  361  TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAAATATTTTATATTTCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTTATTTGTATTAAGATGTTACCACTTTTGACAAAAAGCTTAAAATATTTTATATTTCA  420

Query  421  AAGGAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGGAAAATTAGCAACATAACTTTACAATATATTCTATGATATTTTGATTGTGAGGGCTA  480
```

```
Query  481  CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA  537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCTATTTAAAACTGATGATCTCTGTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA  537
```

# Sequence 381 matched with Sequence 47

```
Query=  Sequence ID - 381               nt:     534
Length=534


   SEQ ID NO: 47            nt:     534

ALIGNMENTS
 Identities = 534/534 (100%), Gaps = 0/534 (0%)

Query  1    GACTTANATCTAAATGGACCACATTCTCTACTTaaaaaaaTGCTATTAACCATGTGATCT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACTTANATCTAAATGGACCACATTCTCTACTTAAAAAAATGCTATTAACCATGTGATCT  60

Query  61   TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTG  120

Query  121  AATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTG  180

Query  181  CTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCCACCC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCCACCC  240

Query  241  TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCT  300

Query  301  TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAA  360

Query  361  AGCAGACAAACAGAAAAAGACATCTTGGGGaaaaaaaCAAGGATAATGGGAAGAGAAGGA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGCAGACAAACAGAAAAAGACATCTTGGGGAAAAAAACAAGGATAATGGGAAGAGAAGGA  420

Query  421  AAGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGA  480
```

```
Query  481  tttttatttttaaaaaaaTAGAAAGCAAAACAAGCTCCTAAAAATAAAGTTTG  534
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTTTATTTTTAAAAAAATAGAAAGCAAAACAAGCTCCTAAAAATAAAGTTTG  534
```

# Sequence 382 matched with Sequence 48

```
Query=  Sequence ID - 382              nt:     444
Length=444


   SEQ ID NO: 48              nt:     444

ALIGNMENTS
 Identities = 444/444 (100%), Gaps = 0/444 (0%)

Query  1    GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTT  60

Query  61   GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGG  120

Query  121  TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACCACGCTGCTTGAG  180

Query  181  GCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCCCTTGCGCCTGCCTCTC  240

Query  241  CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCCTGTTGGCCGAGTGGAGACTGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCCTGTTGGCCGAGTGGAGACTGGT  300

Query  301  GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAACGTTACAACGGAAGTAAAA  360

Query  361  TCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCTGTCGAAATGCACCATGAAGCTTTGAGTGAAGCTTTTCCTGGGGACAATGTGGGCTTC  420

Query  421  AATGTCAAGAATGTGTCTGTCAAG  444
            ||||||||||||||||||||||||
Sbjct  421  AATGTCAAGAATGTGTCTGTCAAG  444
```

# Sequence 383 matched with Sequence 49

```
Query=   Sequence ID - 383                    nt:     566
Length=566


   SEQ ID NO: 49              nt:     566

ALIGNMENTS
 Identities = 566/566 (100%), Gaps = 0/566 (0%)

Query  1     CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA   60

Query  61    GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA   120

Query  121   ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGa   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA   180

Query  181   aaaaaaTGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCC   240

Query  241   CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA   300

Query  301   ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA   360

Query  361   ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA   420

Query  421   ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG   480
```

```
Query  481  TTTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC  540

Query  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
            ||||||||||||||||||||||||||
Sbjct  541  ATTCCTTCAAATAAAGAAATTTGGTA  566
```

# Sequence 384 matched with Sequence 50

```
Query=  Sequence ID 384
Length=400


   SEQ ID NO: 50

ALIGNMENTS
 Identities = 400/400 (100%), Gaps = 0/400 (0%)

Query  1    TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCAGTTA  60

Query  61   GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTCAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATGCATTCAGA  120

Query  121  GATTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTGGCTCACATCTGT  180

Query  181  AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTCAAGAGATAGAGACCAT  240

Query  241  CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTAGTCCCAGCTACTCGGGAGGC  300

Query  301  TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAGGTTTCATTGAGCCGAGATAGTGCC  360

Query  361  ACTGCACTCCAGCCTGGACAACAGAGCGAGACTGTGTCTT    400
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACTGCACTCCAGCCTGGACAACAGAGCGAGACTGTGTCTT    400
```

## Sequence 386 matched with Sequence 51

Query= Sequence ID 386
Length=562


   SEQ ID NO: 51

ALIGNMENTS
 Identities = 562/562 (100%), Gaps = 0/562 (0%)

```
Query  1    CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTTGAGG  60

Query  61   TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAAGAGGGCTG  120

Query  121  CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGTATCTTGGACCAT  180

Query  181  GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAGGAACCAGGGAACATGG  240

Query  241  AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGCTCTAAAGTACTCAGGACTTT  300

Query  301  CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGAGGCTTAAACATAGGGTGACCAACTATCCCACTATGCCTGATACTAAGGGCATTCCC  360

Query  361  TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGGATGTGGACCTTTCATTCCCCAAATTAGGAAAGTCTTGGGCATACCAAGACAAGTTGG  420

Query  421  CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCACCCTACTCAAAAGTATGTAAGCTAACATATCTGTTCTCTAAGAGGTTAAAGCTGGAT  480
```

```
Query   481   GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GGGGATACCAGATGTATGTACGTGATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTAC   540

Query   541   CTGATCGGCCAATTCAATGGGA   562
              ||||||||||||||||||||||
Sbjct   541   CTGATCGGCCAATTCAATGGGA   562
```

## Sequence 387 matched with Sequence 52

```
Query=  Sequence ID 387
Length=614


   SEQ ID NO: 52

ALIGNMENTS
 Identities = 614/614 (100%), Gaps = 0/614 (0%)

Query  1    GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAGA  60

Query  61   AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAGA  120

Query  121  AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGACT  180

Query  181  ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTTGTCTTATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTTGTCTTATT  240

Query  241  AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCCAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCCAGT  300

Query  301  CACTAGGTGAACAACTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACTCATGTCTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACTAGGTGAACAACTTACTGCTCCAATCAGCCTTAGAGCAGGAATCAAACTCATGTCTC  360

Query  361  AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGCTG  420

Query  421  AAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTCTA  480
```

```
Query  481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGG  540

Query  541  TCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGT  600

Query  601  AAATGTGAAGCTTG  614
            ||||||||||||||
Sbjct  601  AAATGTGAAGCTTG  614
```

# Sequence 388 matched with Sequence 53

Query= Sequence ID 388
Length=685


   SEQ ID NO: 53

ALIGNMENTS
 Identities = 685/685 (100%), Gaps = 0/685 (0%)

```
Query  1    CTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGC  60

Query  61   CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCC  120

Query  121  CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGAAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGAAC  180

Query  181  TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAA  240

Query  241  ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCC  300

Query  301  TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTaaaaaaaGTAAAAGGAACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTAAAAAAAGTAAAAGGAACT  360

Query  361  CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGCATCACCAGTATTAGA  420

Query  421  GGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGCGGTACCCTAACCGTGCAAAGGTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGCGGTACCCTAACCGTGCAAAGGTA  480
```

```
Query  481  GCATAATCACTTGTTCCTTAATTAGGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCATAATCACTTGTTCCTTAATTAGGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTG  540

Query  541  TCTCTTACTTTTAACCAGTGAAATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCTCTTACTTTTAACCAGTGAAATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCAA  600

Query  601  GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGG  660

Query  661  TCCTAAACTCCAAACCTGCATTAAA  685
            |||||||||||||||||||||||||
Sbjct  661  TCCTAAACTCCAAACCTGCATTAAA  685
```

# Sequence 389 matched with Sequence 54

Query= Sequence ID 389
Length=533


   SEQ ID NO: 54

ALIGNMENTS
 Identities = 533/533 (100%), Gaps = 0/533 (0%)

```
Query  1    CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTTCCCTTCCCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTTCCCTTCCCG  60

Query  61   TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTC  120

Query  121  CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGCGTCAAGGAAGCT  180

Query  181  GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCACGGACTCTTTCCTCTGAACCCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCACGGACTCTTTCCTCTGAACCCTG  240

Query  241  TTAGGGCTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTAGGGCTTGGTTTTAAAGGATTTTATGTGTGTTTCCGAATGTTTTAGTTAGCCTTTTGG  300

Query  301  TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAATTTGCACATCTCTGGAAGCTTAGC  360

Query  361  AATCTTATTGCACACTGTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATCTTATTGCACACTGTTCGCTGGAAGCTTTTTGAAGAGCACATTCTCCTCAGTGAGCT  420

Query  421  CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CATGAGGTTTTCATTTTTATTCTTCCTTCCAACGTGGTGCTATCTCTGAAACGAGCGTTA  480
```

```
Query  481  GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT  533
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGTGCCGCCTTAGACGGAGGCAGGAGTTTCGTTAGAAAGCGGACGCTGTTCT  533
```

# Sequence 390 matched with Sequence 55

```
Query=   Sequence ID - 390                    nt:     523
Length=523


   SEQ ID NO: 55              nt:     523

ALIGNMENTS
 Identities = 523/523 (100%), Gaps = 0/523 (0%)

Query  1    GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAAACTTAGAACTGCGAAGGAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAAACTTAGAACTGCGAAGGAAT  60

Query  61   GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAAACAAAGAA  120

Query  121  CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGGTTTGGAGCTCCTGAAAGCATCTTTCAAG  180

Query  181  AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGAAAATCAAAGACTGCAA  240

Query  241  AAAACTTTAGAGAACAGCAATAaaaaaaaaTCCAGCAATTAGAGAGTGAACTACAAGACTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAACTTTAGAGAACAGCAATAAAAAAAATCCAGCAATTAGAGAGTGAACTACAAGACTTA  300

Query  301  GAGATGGAAAATCAAACATTGCagaaaaacctagaagaactaaaaatatctagcaaaaga  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGATGGAAAATCAAACATTGCAGAAAAACCTAGAAGAACTAAAAATATCTAGCAAAAGA  360

Query  361  ctagaacagctggaaaaagaaaataaaTCATTAGAGCAAGAGACTTCTCAACTGGAAAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTAGAACAGCTGGAAAAAGAAAATAAATCATTAGAGCAAGAGACTTCTCAACTGGAAAAG  420

Query  421  GATAAGAAACAATTGGAGAAGGAAAATAAGAGACTCCGACANCAAGCAGAAATTAAAGAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GATAAGAAACAATTGGAGAAGGAAAATAAGAGACTCCGACANCAAGCAGAAATTAAAGAT  480
```

```
Query  481   CCACATTTGAAGAAAATAATGTGAAGATTGGAAATTTGGAAAA   523
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCACATTTGAAGAAAATAATGTGAAGATTGGAAATTTGGAAAA   523
```

# Sequence 391 matched with Sequence 56

```
Query=  Sequence ID - 391                  nt:     566
Length=566


   SEQ ID NO: 56              nt:     566

ALIGNMENTS
 Identities = 566/566 (100%), Gaps = 0/566 (0%)

Query  1    CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATGCTGA   60

Query  61   GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGATATCAAGAA   120

Query  121  ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGa   180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGA   180

Query  181  aaaaaaTGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCC   240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAAAATGACCC   240

Query  241  CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGA   300

Query  301  ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTGGGTGACCACGTGACCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGA   360

Query  361  ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATATCTCTTTGACAAGCACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTA   420

Query  421  ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATTTCCCCATAGCCGTGGGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGG   480
```

```
Query  481   TTTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TTTCCTTTACCTTTTCTATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTCC   540

Query  541   ATTCCTTCAAATAAAGAAATTTGGTA   566
             ||||||||||||||||||||||||||
Sbjct  541   ATTCCTTCAAATAAAGAAATTTGGTA   566
```

# Sequence 394 matched with Sequence 57

Query=  Sequence ID 394
Length=616


   SEQ ID NO: 57

ALIGNMENTS
 Identities = 616/616 (100%), Gaps = 0/616 (0%)

```
Query  1    GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCAAGAC  60

Query  61   ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTTAAAATCATTTTATTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTTAAAATCATTTTATTT  120

Query  121  CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTAGTCCTAATATTG  180

Query  181  TATCATTGTGCTGTCTGCAAAACAACTTGAATCTATTTTGTTTGCATCTTTTGTTACATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATCATTGTGCTGTCTGCAAAACAACTTGAATCTATTTTGTTTGCATCTTTTGTTACATG  240

Query  241  TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCATTATGAGAACGCTGTGCTATT  300

Query  301  TACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGTCATGCCTGTGATCCCAGCACTTTG  360

Query  361  GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGAGGCCAAGGTGGGCGGATCACTTGAGGTAAAGAGTTGAGACCAGCCTGGCTAGCATGG  420

Query  421  CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CGAAGCCCAGTCTCTACTAAAAATACAAAAATTGGCCGGGTGAAATTAGCCGGGCGTGGT  480
```

```
Query  481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGTGTGTGCTTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCG  540

Query  541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGAGGCAGAGGTTGCAGTGAGCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAG  600

Query  601  CGAAACTCTGTCTCAA  616
            ||||||||||||||||
Sbjct  601  CGAAACTCTGTCTCAA  616
```

# Sequence 395 matched with Sequence 58

Query=   Sequence ID 395
Length=598


   SEQ ID NO: 58

ALIGNMENTS
 Identities = 598/598 (100%), Gaps = 0/598 (0%)

```
Query  1    CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCCTCCC  60

Query  61   AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTAAATG  120

Query  121  TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGGGAAT  180

Query  181  ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTAGAAT  240

Query  241  CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCATATGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCATATGC  300

Query  301  AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCCTATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCCTATT  360

Query  361  CTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTAAGGA  420

Query  421  GGTCAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGTCAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCTTCACT  480
```

```
Query  481  AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGATTGGT  540

Query  541  AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT  598
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT  598
```

# Sequence 396 matched with Sequence 59

Query=  Sequence ID 396
Length=524


   SEQ ID NO: 59

ALIGNMENTS
 Identities = 524/524 (100%), Gaps = 0/524 (0%)

```
Query   1    CTTAAATCTAAATGGACCACATTCTCTACTTaaaaaaaTGCTATTAACCATGTGATCTTC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CTTAAATCTAAATGGACCACATTCTCTACTTAAAAAAATGCTATTAACCATGTGATCTTC   60

Query   61   TCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTGAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATATTCTTTGAA   120

Query   121  TAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTGCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAGGACAGAGGTGCT   180

Query   181  AGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCCACCCTC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGAGGTAAACCCCACCCTC   240

Query   241  ATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCTTG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  ATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTCTTAAATGTGAGAAATGCTTG   300

Query   301  AAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTAAAGATTTTCATAAAAGAGACCAAA   360

Query   361  GCAGACAAACAGAAAAAGACATCTTGGGGaaaaaaaCAAGGATAATGGGAAGAGAAGGAA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GCAGACAAACAGAAAAAGACATCTTGGGGAAAAAAACAAGGATAATGGGAAGAGAAGGAA   420

Query   421  AGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGAt   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AGTTTTAAAAATTATCAATATCCTCAGGGGGACAAAATATTATATCCTATAAAGACAGAT   480
```

```
Query  481  ttttatttttaaaaaaaTAGAAAGCAAAACAAGCTCCTAAAAA  524
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTTATTTTTAAAAAAATAGAAAGCAAAACAAGCTCCTAAAAA  524
```

# Sequence 397 matched with Sequence 60

Query=   Sequence ID - 397                    nt:      534
Length=534


   SEQ ID NO: 60              nt:      534

ALIGNMENTS
 Identities = 534/534 (100%), Gaps = 0/534 (0%)

```
Query  1    GACCCGGAATCGCGGCCGCGTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCCAAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCCGGAATCGCGGCCGCGTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCCAAAG  60

Query  61   CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAAGAAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAAAAAGAAGG  120

Query  121  AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCCGGAGACAGCCCA  180

Query  181  AATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCACTATGCTATCATCAAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCACTATGCTATCATCAAGT  240

Query  241  TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGACAACAACACACTTGTGTTCA  300

Query  301  TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTGTGGATGTTAAAGCCAACAAGCACCAGATTAAACAGGCTGTGAAGAAGCTGTATGACA  360

Query  361  TTGATGTGGCCAAGGTCAACACCCTGATTCGGCCTGATGGAGAGAAGAAGGCATATGTTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTGATGTGGCCAAGGTCAACACCCTGATTCGGCCTGATGGAGAGAAGAAGGCATATGTTC  420

Query  421  GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GACTGGCTCCTGATTACGATGCTTTGGATGTTGCCAACAAAATTGGGATCATTTAAACTG  480
```

```
Query  481   AGTCCAGCTGCCTAATTCTGAatatatatatatatatatatCTTTTCACCATAA   534
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGTCCAGCTGCCTAATTCTGAATATATATATATATATATATCTTTTCACCATAA   534
```

# Sequence 398 matched with Sequence 61

```
Query=   Sequence ID - 398                    nt:      512
Length=512


   SEQ ID NO: 61              nt:      512

ALIGNMENTS
 Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query  1     GGGGAGCCCCCTCTTCCCTCAGTTGTTCCTACTCAGACTGTTGCACTCTAAACCTAGGGA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGGGAGCCCCCTCTTCCCTCAGTTGTTCCTACTCAGACTGTTGCACTCTAAACCTAGGGA  60

Query  61    GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCTATAGGGTC  120

Query  121   CCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAACATCCCAAGCCAG  180

Query  181   AAAGAAGTTAACTACAGTGTTTTCCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAAGAAGTTAACTACAGTGTTTTCCTTTGCACCGATCCCCACCCCAATTCAATCCCGGAA  240

Query  241   GGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGGCCCCCTGGGCTTGTGAACAC  300

Query  301   CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCCAGCCTCCTGCCTACCCCAAGATG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CTCCTAGCCACATCACTACAGTACAGTGAGTGACCCCAGCCTCCTGCCTACCCCAAGATG  360

Query  361   CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCCCTCCCCACCCTGACCGTGCTAACTGTGTGTACATATATATTCTACATATATGTATAT  420

Query  421   TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAAAACTGCACTGCCATGTCTGCCCTTTTTTGTGGTGTCTAGCATTAACTTATTGTCTAG  480
```

```
Query  481  GCCAAAGCGGGGGTGGGAGGGGAATGCCACAG  512
            ||||||||||||||||||||||||||||||||
Sbjct  481  GCCAAAGCGGGGGTGGGAGGGGAATGCCACAG  512
```

# Sequence 399 matched with Sequence 62

Query=  Sequence ID 399
Length=642


   SEQ ID NO: 62

ALIGNMENTS
 Identities = 642/642 (100%), Gaps = 0/642 (0%)

```
Query  1    TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTTAAAAAACAGCACTTGTTTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTTAAAAAACAGCACTTGTTTTT  60

Query  61   TCTTCCAAGATTAATTTGAAtttttttATGGACATTAGAAAACATTGCAGTTTAGTCATA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTTCCAAGATTAATTTGAATTTTTTTTATGGACATTAGAAAACATTGCAGTTTAGTCATA  120

Query  121  ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTTATTGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTATATTTTTATTGCT  180

Query  181  TACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTGCCACCTTGCACATTCA  240

Query  241  GTGATGTTTGAtttttctttttcctttttttCATATTACTTTTAAATCCTGAATAGTTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTGATGTTTGATTTTTCTTTTTCCTTTTTTTCATATTACTTTTAAATCCTGAATAGTTTG  300

Query  301  TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAACATGGCAATGGTAAGTAATATTGA  360

Query  361  GTAAAGAATAGAAAATTAGTAAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTAAAGAATAGAAAATTAGTAAAATGCATGGCTTCAGAATTATAGCAATTTGCAAAATAG  420

Query  421  GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCCAGCAGATTCTTCTGTTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTAATGGATGAAAATTAGAATGACCAGTTTAACTTTCCCCCCAGCAGATTCTTCTGTTA  480
```

```
Query  481  AACAATGCCCCTTCAAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACAATGCCCCTTCAAAATAAAGGAAGAACAAGTGGGTGTTATACCTATGTTATTTGGCT  540

Query  541  ATGTTAGCACAATATGATGGACTAATTTGAGAAAAAGCATTTACTTCCTTTACTATTACT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATGTTAGCACAATATGATGGACTAATTTGAGAAAAAGCATTTACTTCCTTTACTATTACT  600

Query  601  TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA  642
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCTTTTCTTTATAGGGCTAAGTCTGCCTTCTGGGTCTTTGAA  642
```

# Sequence 400 matched with Sequence 63

```
Query=  Sequence ID 400
Length=446


   SEQ ID NO: 63

ALIGNMENTS
 Identities = 446/446 (100%), Gaps = 0/446 (0%)

Query  1    GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGCGGGC  60

Query  61   CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATGAAAGTCAT  120

Query  121  CATAACAGATGTTTTCCAAAAACTTGTAGAAGGTTGTGAAAAAACTACTAGGATCACGCG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATAACAGATGTTTTCCAAAAACTTGTAGAAGGTTGTGAAAAAACTACTAGGATCACGCG  180

Query  181  GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGCTGTCATGTTTAAAAAT  240

Query  241  ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGGAAGGAAAATTGAAGACGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTTGGAAGGAAAATTGAAGACGT  300

Query  301  GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTTCAAGAAAACATGAACAGAAGCAAATGATGAAAATGAGCATTTTACTTGATGTTGATA  360

Query  361  ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACATCACAATAAATTATGGAGAAAAATACATATTTGGCTAACTTTTAATTGCTGAACAAT  420

Query  421  AAAGTGTTTTCTTTTAAATCNAAAAA    446
            ||||||||||||||||||||||||||
Sbjct  421  AAAGTGTTTTCTTTTAAATCNAAAAA    446
```

# Sequence 401 matched with Sequence 64

Query=   Sequence ID 401
Length=629


   SEQ ID NO: 64

ALIGNMENTS
 Identities = 629/629 (100%), Gaps = 0/629 (0%)

```
Query  1    GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCAGAG   60

Query  61   AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAACTGGAAG   120

Query  121  AAGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATCTGAGTGCCGAC   180

Query  181  TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTTGTCTTAT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTAATGGTGTTGTCTTAT   240

Query  241  TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCCAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTGAGTAATCAGCTAGGCCCAG   300

Query  301  TCACTAGGTGAACAACTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACTCATGTC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCACTAGGTGAACAACTTACTGCTACCAATCAGCCTTAGAGCAGGAATCAAACTCATGTC   360

Query  361  TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCAGAAAAGTTATTAATTCAGCTTGTCTTGGGACTTCCTTCAGAGTCACTCTTGAATAGC   420

Query  421  TGAAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAAATAGTAAATGTTAAATCTGTGGATGCAAGTGTGTAAATTATTTTAGTCATCAGCTC   480
```

```
Query  481  TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAATAAGATGGCCTTTGGGGAAATGAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGA  540

Query  541  GGTCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGTCTACTATTTCTTCTGTAATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTT  600

Query  601  GTAAATGTGAAGCTTGGTCTTTTTCTTTA  629
            |||||||||||||||||||||||||||||
Sbjct  601  GTAAATGTGAAGCTTGGTCTTTTTCTTTA  629
```

## Sequence 402 matched with Sequence 65

Query=   Sequence ID 402
Length=366


   SEQ ID NO: 65

ALIGNMENTS
 Identities = 366/366 (100%), Gaps = 0/366 (0%)

```
Query  1    GACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCC  60

Query  61   TCGTAAGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCGTAAGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATA  120

Query  121  TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTG  180

Query  181  AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATT  240

Query  241  TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCNCAAGAATGAAAGAGGAGGGA  300

Query  301  GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAATGTTTANAGAATAAGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANA  360

Query  361  AAACAG    366
            ||||||
Sbjct  361  AAACAG    366
```

# Sequence 403 matched with Sequence 66

```
Query=   Sequence ID 403
Length=202


   SEQ ID NO: 66


ALIGNMENTS
 Identities = 202/202 (100%), Gaps = 0/202 (0%)

Query  1     AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTTGCCTTCTTACAATCTCAGTGAT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTTGCCTTCTTACAATCTCAGTGAT   60

Query  61    TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGTTGCTGGAT   120

Query  121   ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTTGAATGGGAATTT   180

Query  181   TCTTTATTTCTATANCGTTTNG   202
             ||||||||||||||||||||||
Sbjct  181   TCTTTATTTCTATANCGTTTNG   202
```

Blast comparison trimmed "NG" from the 3' end of both sequences and reported 200 identities. The report has been manually corrected for this. "NG" has been appended to both sequences and identity count has been increased to 202.

## Sequence 405 matched with Sequence 67

Query=   Sequence ID 405
Length=634


   SEQ ID NO: 67

ALIGNMENTS
 Identities = 634/634 (100%), Gaps = 0/634 (0%)

```
Query  1    CCCGGAATCGCGGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTTGGCTGCATAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCGGAATCGCGGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTTGGCTGCATAAA  60

Query  61   TGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTTGATGGGGTTGtttt  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTTGATGGGGTTGTTTT  120

Query  121  tttCTTGTAAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTCTTGTAAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCCTTTGTCAGATGA  180

Query  181  GTAGGTTGCGAAAATTTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTAGGTTGCGAAAATTTTCTCCCATTTTGTAGGTTGCCTGTTCACTCTGATGGTAGTTTC  240

Query  241  ATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTTGTCAATTTTGGCTTTTGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCATTTGTCAATTTTGGCTTTTGT  300

Query  301  TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTTGCCCATGCCTATGTCCTGAATGGT  360

Query  361  AATGCCTAGGTTTTCTTCTAGGGTTTTGATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATGCCTAGGTTTTCTTCTAGGGTTTTGATGGTTTTAGGTCTAACGTTTCAGTCTTTAAT  420

Query  421  CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCATCTTTTAAAAGTCTCTTCACAGTACATGAGTAGTAGTGACACCAATAATGTCAGAGC  480
```

```
Query  481  AGGGAACTCCCAGGTTCTGCCCATCCACAAAAACAACAAATAAGCTGGCAAAAACTTTAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGGGAACTCCCAGGTTCTGCCCATCCACAAAAACAACAAATAAGCTGGCAAAAACTTTAA  540

Query  541  GAATCAACTTTTGCAGATCTCTGAAATCTAGTCAAAACTTAAACAGAGGAAAGATTAATA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAATCAACTTTTGCAGATCTCTGAAATCTAGTCAAAACTTAAACAGAGGAAAGATTAATA  600

Query  601  AAGACNGGCTGCCTGAGATAACACTAACACACAC  634
            |||||||||||||||||||||||||||||||||
Sbjct  601  AAGACNGGCTGCCTGAGATAACACTAACACACAC  634
```

# Sequence 406 matched with Sequence 68

Query=   Sequence ID 406
Length=644


   SEQ ID NO: 68

ALIGNMENTS
 Identities = 644/644 (100%), Gaps = 0/644 (0%)

```
Query   1    CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTTAAATGTTTGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTTAAATGTTTGG   60

Query   61   GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTTGCCAGGGT   120

Query   121  CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCGGGCATT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCACTGTTCGGGCATT   180

Query   181  ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTTCCAAGAATTAAGGATG   240

Query   241  CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTAAAC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  CCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGCAGGCATGCATAAGTGTAAAC   300

Query   301  TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTTTTCAAGGAGTGAATTTCATACCAA   360

Query   361  TCCATTATTATGCTAATAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TCCATTATTATGCTAATAAAAAGGCATGGATCACCAGGGACATCTTTTCAGATTGGTTTC   420

Query   421  ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  ACAAACATTTTGTACCAGCAGCTTGTGCTTACTGCAGGGAAGCTGACTGGATGATGACTG   480
```

```
Query  481  CAAGATTTTGTTATATCTTAACAACTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAAGATTTTGTTATATCTTAACAACTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAA  540

Query  541  AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAATAATGTTTATGGCTCACACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAG  600

Query  601  GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCTNTC  644
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GAGTTCAAGCCCACCCTGGGCAACACAGCAAGACCCAACCTNTC  644
```

Blast comparison trimmed "NTC" from the 3' end of both sequences and reported 641 identities. The report has been manually corrected for this. "NTC" has been appended to both sequences and identity count has been increased to 644.

# Sequence 407 matched with Sequence 69

Query= Sequence ID 407
Length=639


SEQ ID NO: 69

ALIGNMENTS
 Identities = 639/639 (100%), Gaps = 0/639 (0%)

```
Query  1    TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTCTGAA   60

Query  61   CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCCCCAAATGT   120

Query  121  TACAGTGACCACAAAGCAAGGTGTTCACAATAATTACATGGGGGGAATTTTTTAAACCAC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TACAGTGACCACAAAGCAAGGTGTTCACAATAATTACATGGGGGGAATTTTTTAAACCAC   180

Query  181  CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTCAAAATTTCAATGTTAG   240

Query  241  TTTTTGCACGCCCTTccccccccccAACCCTGTTTGTAAGGAACTAAAACATTACATCTGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTTTGCACGCCCTTCCCCCCCCCCAACCCTGTTTGTAAGGAACTAAAACATTACATCTGG   300

Query  301  TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAACAGCAAAGATTTCACTACACCTCAAATGCAGAACACCTATGAAGCAGAGGAATGTT   360

Query  361  GGCTTTTTAAACAGAAGCAGATAaaaaaaaaaaGATGCAGGACTCCTTCAGTTCTTCACTA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGCTTTTTAAACAGAAGCAGATAAAAAAAAAAAGATGCAGGACTCCTTCAGTTCTTCACTA   420

Query  421  GTCTTAGAAAAACTTTCCAGAATACTGCTTCACACTATAaaaaaagaaaaaaTATCTTGCA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTCTTAGAAAAACTTTCCAGAATACTGCTTCACACTATAAAAAAAGAAAAAAATATCTTGCA   480
```

```
Query  481  TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTCGTTTCTAGGAGCACTTTGTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTAGAATCCTTCAACATCTGCATACTGCTTCACACTGTTCGTTTCTAGGAGCACTTTGTC  540

Query  541  ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACAGGACACTTCTGCTTATATTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGT  600

Query  601  GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG  639
            |||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG  639
```

# Sequence 408 matched with Sequence 70

Query=   Sequence ID 408
Length=752


   SEQ ID NO: 70

ALIGNMENTS
 Identities = 752/752 (100%), Gaps = 0/752 (0%)

```
Query   1    CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTTGTTT   60

Query   61   TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGAACAATATT   120

Query   121  GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAAATTCAGCATAACTTTTCCATC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAAATTCAGCATAACTTTTCCATC   180

Query   181  ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTGCTTTCTGTTAGCAGTG   240

Query   241  TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACCACCCGTCATTTTCCCAGAAT   300

Query   301  GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTAGTTGGGAGAGCTGTGGGAGTGAAG   360

Query   361  GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GTCAGGGATGTCACCTACAGAAGTCAGGGAATCTGCCACCAGAGATCCTGCATCAGAAAC   420

Query   421  AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AGCCAACAGCGTGCTTCTGAAGAACTAGTGGGGAAGTGGCTATAATTCTTAGGAATCCCA   480
```

```
Query  481   GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GCAAGTCCGCACCACTGTCTCAGTCTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTC   540

Query  541   TGGAAAGTTCCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TGGAAAGTTCCTGCCCACACTTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAG   600

Query  601   CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CTTCCACACCCAACAAGAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAG   660

Query  661   AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT   720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   AGGGGATTTAGGAGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCT   720

Query  721   TANTTGACAGCGGNCATACACAAATNTNGAAA   752
             |||||||||||||||||||||||||||||||
Sbjct  721   TANTTGACAGCGGNCATACACAAATNTNGAAA   752
```

# Sequence 409 matched with Sequence 71

```
BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.




Query=   Sequence ID 409
Length=12


   SEQ ID NO: 71                                    18.3    2e-04

ALIGNMENTS
 Identities = 12/12 (100%), Gaps = 0/12 (0%)

Query  1    GATCCGTNGACT  12
            ||||||||||||
Sbjct  1    GATCCGTNGACT  12
```

# Sequence 410 matched with Sequence 72

Query=   Sequence ID 410
Length=505


   SEQ ID NO: 72

ALIGNMENTS
 Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query  1     CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTACATGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTACATGG  60

Query  61    CCCTTTCGTGTCTTGGGGGTGGAAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCCTTTCGTGTCTTGGGGGTGGAAAGGGAGGGATGAATTGGGGTGATAGAACCCTGGTGA  120

Query  121   ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAGGATAGGAGTTTA  180

Query  181   GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTAACCATCTGTTTTTTCT  240

Query  241   ACCCTAGCTATCTTTTATTGGTAAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACCCTAGCTATCTTTTATTGGTAAAATATAAATGTATAATTATGTTTGTAGAGCTTTACC  300

Query  301   AAGGAGTTTCCCTCCTTTTTTGTTTGTTGATTAGCAAATTTTTGATTCTCCATTTTCCAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AAGGAGTTTCCCTCCTTTTTTGTTTGTTGATTAGCAAATTTTTGATTCTCCATTTTCCAA  360

Query  361   AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AAGTAAGAGACTCCAGCATGGCCTTCTGTTTGCCCCGCAGTAAAGTAACTTCCATATAAA  420

Query  421   ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTCATCTGTATTTTA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ATGGTATTTGAAAGTGAGAGTTCATGACAACAGACCGTTTTCCATTTCATCTGTATTTTA  480

```
Query  481  TCTCCGTGACTCCACTTGTGGGTTT  505
            |||||||||||||||||||||||||
Sbjct  481  TCTCCGTGACTCCACTTGTGGGTTT  505
```

# Sequence 411 matched with Sequence 73

```
Query=  Sequence ID - 411                    nt:     505
Length=505


   SEQ ID NO: 73            nt:     505

ALIGNMENTS
 Identities = 505/505 (100%), Gaps = 0/505 (0%)

Query  1    TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCGTGTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCGTGTT  60

Query  61   TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAGCACACACA  120

Query  121  ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGTTTATGTATTTAC  180

Query  181  TATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACtttttttttttttttttt  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACTTTTTTTTTTTTTTTTTTT  240

Query  241  GAGATGGAGTTTCACTCTTGTCCTGTAGGCTGGAGCGAANTGGCGCGATCTCGGCTTACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGATGGAGTTTCACTCTTGTCCTGTAGGCTGGAGCGAANTGGCGCGATCTCGGCTTACT  300

Query  301  GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCANCTTCCCAGAGTAGCTGAG  360

Query  361  ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTTGGTAGAGACAGGGTTTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTACAGGCATGCACCGCCACGCACGGGTAATTTTGTATTTTTGGTAGAGACAGGGTTTC  420

Query  421  ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACCATGTTGGCCAGGCTGGTCACCAACTCCTGACCTCAGGTGACCCGCCTCCTCACCTCC  480
```

```
Query  481  AGAGTGTTGGGATTACAGGNGTGAG  505
            |||||||||||||||||||||||||
Sbjct  481  AGAGTGTTGGGATTACAGGNGTGAG  505
```

# Sequence 412 matched with Sequence 74

Query=   Sequence ID 412
Length=580


   SEQ ID NO: 74

ALIGNMENTS
 Identities = 580/580 (100%), Gaps = 0/580 (0%)

```
Query  1    ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGTAGGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGTAGGA  60

Query  61   GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCC  120

Query  121  AGCCTGTGTGACAGAACAAGACTCTGTCTCaaaaaaaaataataataataataataataa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAATAATAATAATAATAATAATAA  180

Query  181  aaaggaataacatagctaggaataaatttaatCAAAGAGGTGAAAGACTTATACACTTAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTATACACTTAA  240

Query  241  AACTACaaaaaaaaaaTCACTGAAGGAATTATAGACCCaaataaaaataaataaaaaGAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAGAC  300

Query  301  ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGTG  360

Query  361  ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAA  420

Query  421  AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAACACAATCTT  480
```

```
Query  481  GGGGaaaaaaaacaaaaaacaaaGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGAAAAAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAATTTACTA  540

Query  541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAAGTTATAGNATCAAAGTCGACGCGCCGCGATCCGGGC  580
```

# Sequence 413 matched with Sequence 75

Query= Sequence ID 413
Length=535


   SEQ ID NO: 75

ALIGNMENTS
 Identities = 535/535 (100%), Gaps = 0/535 (0%)

```
Query  1    CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA  60

Query  61   AATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTaaaaaaaGTAAAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAAAGTAAAAT  120

Query  121  CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTAACAAAAGAAAG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTAACAAAAGAAAG   180

Query  181  AAAACAACttttttttAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC  240

Query  241  ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT  300

Query  301  GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG  360

Query  361  ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA  420

Query  421  AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA  480
```

```
Query  481  ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTTGTTCTAT  535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTTGTTCTAT  535
```

# Sequence 414 matched with Sequence 76

Query=  Sequence ID 414
Length=505


   SEQ ID NO: 76

ALIGNMENTS
 Identities = 505/505 (100%), Gaps = 0/505 (0%)

```
Query  1    CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGGACCC  60

Query  61   ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCAGGCAGCCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCAGGCAGCCT  120

Query  121  GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTGTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCCCCCTCCCTTGTG  180

Query  181  GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAAGAAGCTAAAGCTAAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAAGAAGCTAAAGCTAAAG  240

Query  241  AAACCTTCCTTTTTTCAACGtttttttttCTTTCAAACTGTAGGGTCACTTTTGATTGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAACCTTCCTTTTTTCAACGTTTTTTTTTCTTTCAAACTGTAGGGTCACTTTTGATTGAG  300

Query  301  GCAAAGGGGTCCTACTGTAAGTGGAAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCAAAGGGGTCCTACTGTAAGTGGAAAAGACTCACTCCCCTAACATAAGTTTTCACTGTG  360

Query  361  GTGGGATGGTGCCGCCCGATATGCTTGATATGCTTTTCCTTCCACATGTTAAGCTAGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTGGGATGGTGCCGCCCGATATGCTTGATATGCTTTTCCTTCCACATGTTAAGCTAGGAA  420

Query  421  ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACCTAACAGGATGTCAGCAGGGCAGTTAACTCTGGACTCANAGCCCTCAAGGGCATGTGG  480
```

```
Query  481  CANAACCTCATGGCATNCAAGACCA  505
            |||||||||||||||||||||||||
Sbjct  481  CANAACCTCATGGCATNCAAGACCA  505
```

## Sequence 415 matched with Sequence 77

```
Query=   Sequence ID - 415                   nt:     596
Length=596


   SEQ ID NO: 77            nt:     596

ALIGNMENTS
 Identities = 596/596 (100%), Gaps = 0/596 (0%)

Query  1     GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGaaaaaaaTTATCCA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGAAAAAAATTATCCA   60

Query  61    AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCACATGGAAAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCACATGGAAAT   120

Query  121   GTATGAACCATGACCTCTATGTCACATACTATATATAAAACTTAATTTGAGGTGTATCAC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTATGAACCATGACCTCTATGTCACATACTATATATAAAACTTAATTTGAGGTGTATCAC   180

Query  181   AGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCCGCACAAGAGATGTCTG   240

Query  241   CATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAACATGCAAAAAGCACTAACTG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAACATGCAAAAAGCACTAACTG   300

Query  301   TAAAAGAGAACAGTTGGTCAGTTGAATTTCATGAAACATTGTAAACTTCTGCTAAACAAC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAAAAGAGAACAGTTGGTCAGTTGAATTTCATGAAACATTGTAAACTTCTGCTAAACAAC   360

Query  361   TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TGACACCATTAAGAATGTGGAAAAAGGCTGGGCACAGTGGCTCATGCCTATAATCCCAGC   420

Query  421   ATTTTGGGAGGCCGGGGCGGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ATTTTGGGAGGCCGGGGCGGGAGAATCACTTGAGGCCAGGAGTTTGAAACCAGCCTGGGC   480
```

```
Query  481   AACATGGCAAGACCCCGACTCTACAAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AACATGGCAAGACCCCGACTCTACAAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATG   540

Query  541   CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGGNGGAAGGATCACTTAACCCTGG   596
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CACTCCTGTAGTCCTAGCTGCCAGGANGCTAAGGNGGAAGGATCACTTAACCCTGG   596
```

# Sequence 416 matched with Sequence 78

Query=   Sequence ID 416
Length=504


    SEQ ID NO: 78

ALIGNMENTS
 Identities = 504/504 (100%), Gaps = 0/504 (0%)

Query  1    CTGGTGGCGGCGGTCGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGGTGGCGGCGGTCGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACTGGCA  60

Query  61   AAACCATCACCCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAACCATCACCCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGCCAAAATTC  120

Query  121  AAGACAAGGAGGGTATCCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGACAAGGAGGGTATCCCACCTGACCAGCAGCGTCTGATATTTGCCGGCAAACAGCTGG  180

Query  181  AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCCACCCTGCACCTGGTGT  240

Query  241  TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCCAGAAATACAACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCAGCTTGCCCAGAAATACAACT  300

Query  301  GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTCACCCTCGTGCTGTCAACTGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCCTTCACCCTCGTGCTGTCAACTGCC  360

Query  361  GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCAAGAAGAAGTGTGGTCACACCAACAACCTGCGTCCCAAGAAGAAGGTCAAATAAGGTT  420

Query  421  GTTCTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCCGTGGCCCTGGAGCCTCAATAAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTCTTTCCTTGAAGGGCAGCCTCCTGCCCAGGCCCCGTGGCCCTGGAGCCTCAATAAAG  480

```
Query  481  TGTCCCTTTCATTGACTGGAGCAG  504
            ||||||||||||||||||||||||
Sbjct  481  TGTCCCTTTCATTGACTGGAGCAG  504
```

# Sequence 417 matched with Sequence 79

Query=  Sequence ID 417
Length=564


   SEQ ID NO: 79

ALIGNMENTS
 Identities = 564/564 (100%), Gaps = 0/564 (0%)

```
Query   1    GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGtttttttt  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGTTTTTTTT  60

Query   61   CTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAG   120

Query   121  ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT   180

Query   181  ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACG   240

Query   241  GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA   300

Query   301  AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAA   360

Query   361  GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG   420

Query   421  GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC   480
```

```
Query  481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAAATGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACCAAAATGG  540

Query  541  AAAGATTAATTGGGAGTGGTAGGA  564
            ||||||||||||||||||||||||
Sbjct  541  AAAGATTAATTGGGAGTGGTAGGA  564
```

# Sequence 418 matched with Sequence 80

Query=  Sequence ID 418
Length=270


   SEQ ID NO: 80

ALIGNMENTS
 Identities = 270/270 (100%), Gaps = 0/270 (0%)

```
Query  1     CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA   60

Query  61    TGCAAAAtttttttaatcttcgccttaatactttttttattttgttttattttGAATGATG   120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGCAAAATTTTTTTAATCTTCGCCTTAATACTTTTTTTATTTTGTTTTATTTTGAATGATG   120

Query  121   AGCCTTCGTGccccccccttcccccttttttgtcccccAACTTGAGATGTATGAAGGCTTT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AGCCTTCGTGCCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATGTATGAAGGCTTT   180

Query  181   TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA   240

Query  241   GTTGAATAAAAGTGCACACCTTATAAAAAA   270
             ||||||||||||||||||||||||||||||
Sbjct  241   GTTGAATAAAAGTGCACACCTTATAAAAAA   270
```

# Sequence 419 matched with Sequence 81

```
Query=   Sequence ID 419
Length=268


   SEQ ID NO: 81

ALIGNMENTS
 Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query  1    CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTATGTAA  60

Query  61   TGCAAAAtttttttaatcttcgccttaatacttttttattttgttttattttGAATGATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGCAAAATTTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTTGAATGATG  120

Query  121  AGCCTTCGTGccccccccttcccccttttttgtcccccAACTTGAGATGTATGAAGGCTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCCTTCGTGCCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATGTATGAAGGCTTT  180

Query  181  TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTACACTGACTTGAGACCA  240

Query  241  GTTGAATAAAAGTGCACACCTTATAAAA  268
            ||||||||||||||||||||||||||||
Sbjct  241  GTTGAATAAAAGTGCACACCTTATAAAA  268
```

# Sequence 420 matched with Sequence 82

Query=  Sequence ID 420
Length=334


   SEQ ID NO: 82

ALIGNMENTS
 Identities = 334/334 (100%), Gaps = 0/334 (0%)

```
Query  1    CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGGAACT  60

Query  61   GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTACAAACCCC  120

Query  121  GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAATCAGAATGGTAAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAATCAGAATGGTAAA  180

Query  181  TTGATTAAATGCTCCTAACCCTGTAATTTTGTGCATAGAGCACCCTATGCTGTGGAAATA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGATTAAATGCTCCTAACCCTGTAATTTTGTGCATAGAGCACCCTATGCTGTGGAAATA  240

Query  241  ACTGTTCTTAGATTTCATTGTAACTGGACTGTTCAGGTTGCCCAGAGGGAAAGAACATTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTGTTCTTAGATTTCATTGTAACTGGACTGTTCAGGTTGCCCAGAGGGAAAGAACATTC  300

Query  301  CTAATTCTAATAAAATAAACTTTTATTTTGTTTA  334
            |||||||||||||||||||||||||||||||||
Sbjct  301  CTAATTCTAATAAAATAAACTTTTATTTTGTTTA  334
```

# Sequence 421 matched with Sequence 83

```
Query=   Sequence ID 421
Length=675


   SEQ ID NO: 83

ALIGNMENTS
 Identities = 675/675 (100%), Gaps = 0/675 (0%)

Query  1     TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGGTGCA  60

Query  61    CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTCAGCATTCCGTGGAATTTGTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTCAGCATTCCGTGGAATTTGTA  120

Query  121   CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTCACAAAGATTTGTTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTCACAAAGATTTGTTT  180

Query  181   TTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAATACTTTAATTATAAAAA  240

Query  241   GTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAAT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTTTAAAATGTATATTTCTTAAT  300

Query  301   ATCTTGAAATTGTAATGCCtttttttttttcctaaatttttttttGTCATGAAATGAGATAG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAATTTTTTTTGTCATGAAATGAGATAG  360

Query  361   TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TAACAGCAGATTGGGACAACAAGGTTATATTCTTGTCTTGAATCAGGCCATGGCTTCTTT  420

Query  421   CATCCAAATTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CATCCAAATTTCAGACCTCATTTATTTACTTTGTCCCTGCCTCCCATCCCTGGATATCAG  480
```

```
Query  481  TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTGTGGATATCTACAGTTAATAGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCT  540

Query  541  GAATAAAATCTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAATAAAATCTTTGAATCAGATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAA  600

Query  601  TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTGCTCTAATTTTGAGAGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATAT  660

Query  661  GTAGACATTTTAATT  675
            |||||||||||||||
Sbjct  661  GTAGACATTTTAATT  675
```

# Sequence 422 matched with Sequence 84

```
Query=   Sequence ID 422
Length=485


   SEQ ID NO: 84

ALIGNMENTS
 Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query  1     GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTGGCCA  60

Query  61    GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTCTGGGGCTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTCTGGGGCTG  120

Query  121   TGATCCTGCGATGGTGCCTGGGTGGGAGTgggggtgggggGCGGGATGGTCTCCCTACCT  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGATCCTGCGATGGTGCCTGGGTGGGAGTGGGGGTGGGGGGCGGGATGGTCTCCCTACCT  180

Query  181   GCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT  240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANACTTGGCTCCTGTCCAT  240

Query  241   GTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAAGANAGAGACGGGTGGTGTANGGC  300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAAGANAGAGACGGGTGGTGTANGGC  300

Query  301   ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC  360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGANAATGGAAACAGGCGAAACTTACC  360

Query  361   AAGTGTAACATCACCTGGAACTGAAGGAGGGTGGGAAGGTTTTAATTATTTTAAAAATAG  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AAGTGTAACATCACCTGGAACTGAAGGAGGGTGGGAAGGTTTTAATTATTTTAAAAATAG  420

Query  421   AGATGGGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACTACTGGGCTCAAGTGAACCTC  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AGATGGGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACTACTGGGCTCAAGTGAACCTC  480
```

```
Query  481  CTTCT  485
            |||||
Sbjct  481  CTTCT  485
```

# Sequence 423 matched with Sequence 85

```
Query=  Sequence ID - 423                    nt:    387
Length=387


   SEQ ID NO: 85              nt:    387

ALIGNMENTS
 Identities = 387/387 (100%), Gaps = 0/387 (0%)

Query  1    TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCATGAGA  60

Query  61   AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAGACTCACAGAGGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAGACTCACAGAGGG  120

Query  121  CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCANAAGGGTTCTGA  180

Query  181  ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCCTCTTTTCCTCACAGCAATTCTGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCCTCTTTTCCTCACAGCAATTCTGA  240

Query  241  CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCAGGGTATGAATGACCATCAGC  300

Query  301  CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCACCCAAGCTGCTGTGGCCCAGACTGG  360

Query  361  TGACATCACCTCAGGGCaaaaaaaaaa  387
            |||||||||||||||||||||||||||
Sbjct  361  TGACATCACCTCAGGGCAAAAAAAAAA  387
```

# Sequence 424 matched with Sequence 86

```
Query=  Sequence ID - 424                nt:      420
Length=420


   SEQ ID NO: 86             nt:      420

ALIGNMENTS
 Identities = 420/420 (100%), Gaps = 0/420 (0%)

Query  1    CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCATCAAC  60

Query  61   GAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAGTGGGCTTC  120

Query  121  AAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGA  180

Query  181  ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTGGGCCAAAGGAATAAGG  240

Query  241  AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAACGTAATGAGGATGAAGATTCA  300

Query  301  CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCAAATAAGCTATATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAG  360

Query  361  ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACAGTCAATGTGGATGAGAACTAATCGCTGATCGTCAGATCAAATAAAGTTATAAAATTG  420
```

# Sequence 425 matched with Sequence 87

Query= Sequence ID 425
Length=675


   SEQ ID NO: 87

ALIGNMENTS
 Identities = 675/675 (100%), Gaps = 0/675 (0%)

```
Query  1    GGAAACTGATGCCAGTCAGAAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAATTGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAACTGATGCCAGTCAGAAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAATTGA  60

Query  61   TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGAAAGACAGT  120

Query  121  TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGTAAAAGATCGTGA  180

Query  181  AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTTGTAAGATGATGAACTT  240

Query  241  ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATATATATTGTAATCCCTAGAGC  300

Query  301  AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAGGTGATAAAATGGAATACTAAAAAA  360

Query  361  TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TATCAGATGAATAATAAAGAAGACAGGAAATGAGGAACAGTGGAACAGAATGAATAAAAA  420

Query  421  ACAAGACCATTAACTTAATCATTAATAATTACTTTAAATGGGTTAAACATTATGGTTATA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACAAGACCATTAACTTAATCATTAATAATTACTTTAAATGGGTTAAACATTATGGTTATA  480
```

```
Query   481  AGGCAGAGATTTTCAGACTAGATAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AGGCAGAGATTTTCAGACTAGATAAAAGAGCAAGCTCCACTATATACTGTCTACAAGAGA   540

Query   541  TATACTTTAAAGTGTATATTATATTTAAATATAAAGATTTGGAATAAATAAACCTAAGAA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATACTTTAAAGTGTATATTATATTTAAATATAAAGATTTGGAATAAATAAACCTAAGAA   600

Query   601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TAAGCTTACTAGGGAAGTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGA   660

Query   661  AATCATAGGTGACCA   675
             |||||||||||||||
Sbjct   661  AATCATAGGTGACCA   675
```

# Sequence 426 matched with Sequence 88

Query=  Sequence ID 426
Length=594


   SEQ ID NO: 88

ALIGNMENTS
 Identities = 594/594 (100%), Gaps = 0/594 (0%)

```
Query  1    GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGTCAGG  60

Query  61   CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCTTTGTAGGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCTTTGTAGGG  120

Query  121  CTAACAGTGTTGCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTAACAGTGTTGCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTTTCCTACCTTATT  180

Query  181  CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAATGGTATGGAAATGAGA  240

Query  241  TTGTAATGTCATTATTTCCTCTTTAAATAATCAGGACAACTCATGATACAAAGAGCTCTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGTAATGTCATTATTTCCTCTTTAAATAATCAGGACAACTCATGATACAAAGAGCTCTT  300

Query  301  CTCTATAAAAGGTGGGACtttttttttttAGTAATAGCAAAAATAAAATTGTACCTCCTTA  360
            ||||||||||||||||||||           |||||||||||||||||||||||||||||||
Sbjct  301  CTCTATAAAAGGTGGGACTTTTTTTTTTAGTAATAGCAAAAATAAAATTGTACCTCCTTA  360

Query  361  ATCTTCTACAGAAAGATGGATTTCATTTTCAACATTAAGAGGTAGTTTTAAGAAGCAGTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCTTCTACAGAAAGATGGATTTCATTTTCAACATTAAGAGGTAGTTTTAAGAAGCAGTA  420

Query  421  GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAGTCAGCCTGGGCAGCATGGTGAAACCCCGTCTCTACAAAAAAGTTAGCTGGGCTTAG  480
```

```
Query  481   TAGTTGCAATCCCAGCTACTCTGGAGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  481   TAGTTGCAATCCCAGCTACTCTGGAGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGT   540

Query  541   CNAGGCTGCAATGATACANTGAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA   594
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CNAGGCTGCAATGATACANTGAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA   594
```

## Sequence 427 matched with Sequence 89

Query=  Sequence ID 427
Length=530


   SEQ ID NO: 89

ALIGNMENTS
 Identities = 530/530 (100%), Gaps = 0/530 (0%)

```
Query  1    TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGGGTAT  60

Query  61   GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAGTGTGTACC  120

Query  121  ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCAATGGGGCTGGAC  180

Query  181  ACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACATGCTTAAAAACGCAGA  240

Query  241  GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTGGTCATTGAGCATATCCAAGT  300

Query  301  GAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCGGATTAACCCATA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACAAAGCACCTAAGATGCGCCGCCGGACCTACAGAGCTCATGGTCGGATTAACCCATA  360

Query  361  CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CATGAGCTCTCCCTGCCACATTGAGATGATCCTTACGGAAAAGGAACAGATTGTTCCTAA  420

Query  421  ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACCAGAAGAGGAGGTTGCCCAGAAGAAAAAGATATCCCAGAAGAAACTGAAGAAACAAAA  480
```

```
Query  481   ACTTATGGCACGGGAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGG   530
             |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ACTTATGGCACGGGAGTAAATTCAGCATTAAAATAAATGTAATTAAAAGG   530
```

# Sequence 428 matched with Sequence 90

```
Query=   Sequence ID 428
Length=381


   SEQ ID NO: 90

ALIGNMENTS
 Identities = 381/381 (100%), Gaps = 0/381 (0%)

Query  1    TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGAATTT  60

Query  61   TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAAAGAAATTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAAAGAAATTA  120

Query  121  GAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTACAATGCTCAAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTACAATGCTCAAAT  180

Query  181  GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTGAAATTAACCCTGCAGC  240

Query  241  ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCCAGCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGAGGATAGCCAGGTGCCCAGCA  300

Query  301  TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGCTTCTTCGAAACGTCACCCTGCCAG  360

Query  361  AAATATTCTGAGACCAAATTT  381
            |||||||||||||||||||||
Sbjct  361  AAATATTCTGAGACCAAATTT  381
```

# Sequence 429 matched with Sequence 91

Query= Sequence ID - 429                  nt:     535
Length=535


   SEQ ID NO: 91              nt:     535

ALIGNMENTS
 Identities = 535/535 (100%), Gaps = 0/535 (0%)

```
Query  1    CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACACGAA  60

Query  61   AATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTaaaaaaaGTAAAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAAAGTAAAAT  120

Query  121  CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTAACAAAAGAAAG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTAACAAAAGAAAG   180

Query  181  AAAACAACtttttttAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATGTACCTTATTCCCACAC  240

Query  241  ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATATTACTTTGTTTAAAATAAGAT  300

Query  301  GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAATTTAAAAACTCCTCTTCACGATTG  360

Query  361  ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATAGCAAAATCAGAAACGTTAGGGCACCAGTGAGTTGAAAAAACTGGTCTTAAGTTGGAA  420

Query  421  AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAACTATTATTAATAATATTATCCTATCCATCCATATCTATTGAAATTGTCAGGTCCATA  480
```

```
Query  481  ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTTGTTCTAT  535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTCATTTTAATTAATTATAGGAAAGAAGAAAAGATAATACCCATTTGTTCTAT  535
```

# Sequence 430 matched with Sequence 92

Query=  Sequence ID 430
Length=619


   SEQ ID NO: 92

ALIGNMENTS
 Identities = 619/619 (100%), Gaps = 0/619 (0%)

```
Query  1    CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttttttttCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||      ||
Sbjct  1    CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTTCT  60

Query  61   CTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAGAT  120

Query  121  ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATAT  180

Query  181  GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGA  240

Query  241  GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAG  300

Query  301  GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGG  360

Query  361  TGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAGGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAGGC  420

Query  421  GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAG  480
```

```
Query  481  GGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAA  540

Query  541  AGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAA  600

Query  601  ACTGGAAGACAGAAGTACC  619
            |||||||||||||||||||
Sbjct  601  ACTGGAAGACAGAAGTACC  619
```

# Sequence 431 matched with Sequence 93

```
Query=   Sequence ID 431
Length=131
```

```
   SEQ ID NO: 93
```

```
ALIGNMENTS
 Identities = 131/131 (100%), Gaps = 0/131 (0%)

Query  1    CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTGTTGT  60

Query  61   AAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTnaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGTTNAAAAAA  120

Query  121  aaaaaaNANCA  131
            |||||||||||
Sbjct  121  AAAAAANANCA  131
```

Blast comparison trimmed "NANCA" from the 3' end of both sequences and reported 126
identities. The report has been manually corrected for this. "NANCA" has been appended
to both sequences and identity count has been increased to 131.

## Sequence 432 matched with Sequence 94

Query=  Sequence ID 432
Length=607


   SEQ ID NO: 94

ALIGNMENTS
 Identities = 607/607 (100%), Gaps = 0/607 (0%)

```
Query  1    TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGGTCCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGGTCCA  60

Query  61   AGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCAGAGACTCT  120

Query  121  CCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGGAATGCTTATAGG  180

Query  181  AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTTGGTCCAGTGCAACCCT  240

Query  241  TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAAGAACCATCTGGAAACACACC  300

Query  301  AGCTTCTGCTACCTTCATGCTCATTGTTaaaaaaaGATTAACCAGTGTGAACATTCTGAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAAGATTAACCAGTGTGAACATTCTGAT  360

Query  361  CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTGTTAATTCCAGGGACTGTTTTCTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCA  420

Query  421  AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAGCTCAAAGCTAAAATGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGG  480
```

```
Query  481  CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGGCGTGGTTGAGCTGATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGC  540

Query  541  TATCCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATCCCACCCCAAATTTCAACCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCT  600

Query  601  CAGAGCA  607
            |||||||
Sbjct  601  CAGAGCA  607
```

# Sequence 433 matched with Sequence 95

Query=   Sequence ID 433
Length=687


   SEQ ID NO: 95

ALIGNMENTS
 Identities = 687/687 (100%), Gaps = 0/687 (0%)

```
Query   1    TCCCGGAATCGCGGCCGCGTCGACCCGCCGCCGAGGATTCAGCAgcctcccccttgagcc   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TCCCGGAATCGCGGCCGCGTCGACCCGCCGCCGAGGATTCAGCAGCCTCCCCCTTGAGCC   60

Query   61   ccctcgcttcccgacgttccgttcccccctgcccgccttctcccgccaccgccgccgccg   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CCCTCGCTTCCCGACGTTCCGTTCCCCCCTGCCCGCCTTCTCCCGCCACCGCCGCCGCCG   120

Query   121  ccttccgcaggccgTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CCTTCCGCAGGCCGTTTCCACCGAGGAAAAGGAATCGTATCGTATGTCCGCTATCCAGAA   180

Query   181  CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATGACCTGCTTCCTGCTGG   240

Query   241  CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  CACTGAGGATTATATCCATATAAGAATTCAACAGAGAAACGGCAGGAAGACCCTTACTAC   300

Query   301  TGTCCAAGGGATCGCTGATGATTACGATAAAAAGAAACTAGTGAAGGCGTTTAAGAAAAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TGTCCAAGGGATCGCTGATGATTACGATAAAAAGAAACTAGTGAAGGCGTTTAAGAAAAA   360

Query   361  GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GTTTGCCTGCAATGGTACTGTAATTGAGCATCCGGAATATGGAGAAGTAATTCAGCTACA   420

Query   421  GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GGGTGACCAACGCAAGAACATATGCCAGTTCCTCGTAGAGATTGGACTGGCTAAGGACGA   480
```

```
Query  481  TCAGCTGAAGGTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCAGCTGAAGGTTCATGGGTTTTAAGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTT  540

Query  541  CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCTTGCAATGAGTAGAATTTCCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTT  600

Query  601  GTATAATGTAACCATTTGGGGTCCGCTTTTAACTTGGACTAGTGTAACTNCTTCATGCAA  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GTATAATGTAACCATTTGGGGTCCGCTTTTAACTTGGACTAGTGTAACTNCTTCATGCAA  660

Query  661  TAAACTGAAAAGACCATGCTGCTANTC   687
            |||||||||||||||||||||||||||
Sbjct  661  TAAACTGAAAAGACCATGCTGCTANTC   687
```

Blast comparison trimmed "NTC" from the 3' end of both sequences and reported 684 identities. The report has been manually corrected for this. "NTC" has been appended to both sequences and identity count has been increased to 687.

## Sequence 434 matched with Sequence 96

```
Query=  Sequence ID 434
Length=462
```

```
   SEQ ID NO: 96
```

```
ALIGNMENTS
 Identities = 462/462 (100%), Gaps = 0/462 (0%)
```

```
Query  1    TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCTCATC  60

Query  61   AAGGTGAACGGGCGGCCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGGTGAACGGGCGGCCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACAAGCTGCTG  120

Query  121  GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATCCGTGTCCGTGTA  180

Query  181  AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTCCATCTCCAAAGCCCTG  240
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  181  AAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTCCATCTCCAAAGCCCTG  240

Query  241  GTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC  300
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGAAGGAGATCAAAGACATCCTC  300

Query  301  ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCTCGTCGCTGCGAGTCCAAAAAGTTT  360

Query  361  GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGAGGCCCTGGTGCCCGCGCTCGCTACCAGAAATCCTACCGATAAGCCCATCGTGACTCA  420

Query  421  AAACTCACTTGTATAATAAACAGTTTTTGAGGGATTTTAAAA  462
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAACTCACTTGTATAATAAACAGTTTTTGAGGGATTTTAAAA  462
```

# Sequence 435 matched with Sequence 97

Query= Sequence ID 435
Length=535


   SEQ ID NO: 97

ALIGNMENTS
 Identities = 535/535 (100%), Gaps = 0/535 (0%)

```
Query  1    CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAACCTAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAACCTAT  60

Query  61   CTCTTaaaaaaaaaaaaaaaaaaaaGGAAGAAGAGACATGAGAGGGCCCAAGTCACTTGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCTTAAAAAAAAAAAAAAAAAAAAGGAAGAAGAGACATGAGAGGGCCCAAGTCACTTGCT  120

Query  121  CACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGAGCAAGAAGGCAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGAGCAAGAAGGCAG  180

Query  181  CCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAAACTGAGCCAGAACCTTGGAATTCCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAAACTGAGCCAGAACCTTGGAATTCCA  240

Query  241  GCCTCCANAACTGTGAGAAAAGAATTTTCTGTTGTTTCAGTCCCCCACACTATGGCATTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCCTCCANAACTGTGAGAAAAGAATTTTCTGTTGTTTCAGTCCCCCACACTATGGCATTT  300

Query  301  TGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTCCTGCATTTACTTGGTCTTCCAGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTCCTGCATTTACTTGGTCTTCCAGTT  360

Query  361  AGTTTTTTAGACTTTGGGAATCAGAGCAGTCAGTTGTCAGATTTTAGCTTACAGTTGTCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTTTTTTAGACTTTGGGAATCAGAGCAGTCAGTTGTCAGATTTTAGCTTACAGTTGTCC  420

Query  421  TACCTGTGCAACTGAAATTTCTTCCATTTTAAACCAGAGCAGAGTTTTAGAGTCAAAAGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACCTGTGCAACTGAAATTTCTTCCATTTTAAACCAGAGCAGAGTTTTAGAGTCAAAAGA  480
```

```
Query  481   AACCAGATCTTTTAGTGCAGAAGCTTTCCACTGTATTANAAGTGAGGAAGTTGGT   535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AACCAGATCTTTTAGTGCAGAAGCTTTCCACTGTATTANAAGTGAGGAAGTTGGT   535
```

# Sequence 436 matched with Sequence 98

Query=  Sequence ID 436
Length=512


   SEQ ID NO: 98

ALIGNMENTS
 Identities = 512/512 (100%), Gaps = 0/512 (0%)

```
Query  1    aaaaaaaCTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAAAAAACTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAATAGT  60

Query  61   TTCATTTGTTAGAATATAATTGTCTTCCACTaaaaaaagaaaaaaaaaaGCATTTAAGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTCATTTGTTAGAATATAATTGTCTTCCACTAAAAAAAGAAAAAAAAAAAGCATTTAAGGC  120

Query  121  TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTATGTGCATTATTTT  180

Query  181  TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAGCTTTCCATTATGAATT  240

Query  241  CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAATTTACAATAGTTTATATATG  300

Query  301  CAAATATTATGTTGTTAGAGTTGGTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAAATATTATGTTGTTAGAGTTGGTTTTCATGTCATTTTTACATATACAGGGGCAGTTTC  360

Query  361  CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTTCTGTGTCAATTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCAACTAAATTGTATATTCCTTAAAGCAGCACTCTTAAATTTTATTTCTGTGTCAATTT  420

Query  421  CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTGNCTGTGTTTCCTGGCATGGAATACATGGCATAAAATTTGTTATGTAATTAAATGAA  480
```

```
Query  481  ATATTATTATACTTTCTATTTTTTAGAAAAAA  512
            ||||||||||||||||||||||||||||||||
Sbjct  481  ATATTATTATACTTTCTATTTTTTAGAAAAAA  512
```

## Sequence 438 matched with Sequence 99

```
Query=  Sequence ID - 438                    nt:     577
Length=577


   SEQ ID NO: 99              nt:     577

ALIGNMENTS
 Identities = 577/577 (100%), Gaps = 0/577 (0%)

Query  1     GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACTCTGG  60

Query  61    GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCATGCACCGCC  120

Query  121   ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGTCAGGCTGGTCTC  180

Query  181   GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACCACAGAC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAGTCCTGGAACCACAGAC  240

Query  241   ATGAGCCACCACGCCTGGCCCCTTTTAAAATATTTCTGCTCATTGATGATGCACCCAGTC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ATGAGCCACCACGCCTGGCCCCTTTTAAAATATTTCTGCTCATTGATGATGCACCCAGTC  300

Query  301   ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGAATGCTGTTTTCATGGCTGCTAATA  360

Query  361   CAACATTCATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CAACATTCATTCTGCAACCCCCAAATCAAGAAGTAATTTTGACTTTCAAGTCTTATTATT  420

Query  421   TAAGAAATATATTTTGCAAGACTATAGCTGCCATAGACCGTGATTCCTCTGATGGATCAG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAAGAAATATATTTTGCAAGACTATAGCTGCCATAGACCGTGATTCCTCTGATGGATCAG  480
```

```
Query  481  ACAAACTAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACAAACTAAAATGAAAACCTCCTGCAACGTATTCATCATTCTAGATCCCTGAGGAATCGC  540

Query  541  CACACTGACTTNCACAATGGGTGAACTGGGTTACAGT  577
            |||||||||||||||||||||||||||||||||||||
Sbjct  541  CACACTGACTTNCACAATGGGTGAACTGGGTTACAGT  577
```

# Sequence 441 matched with Sequence 100

Query=  Sequence ID - 441                    nt:     552
Length=552


   SEQ ID NO: 100              nt:     552

ALIGNMENTS
 Identities = 552/552 (100%), Gaps = 0/552 (0%)

Query  1    AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCCCATA  60

Query  61   AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGGACATCTCT  120

Query  121  GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GACCATCCATCGCTGTATTCAAATGGATTGTTTTATTCCATTCTGGTCTCAGGCATGACC  180

Query  181  ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGGCAATAGACTGGCCCCA  240

Query  241  ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTTGTGTGGAACAGCTCACCTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTTGTGTGGAACAGCTCACCTTG  300

Query  301  TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGCAGAAAATGACATTCATCTTTTGAG  360

Query  361  TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCCTCATCCATGGAGTGCTGTGTTTGGGGGGCTGCATCTGCTGAAGCGAGAACCCCATTC  420

Query  421  TGCCACCCCACCAGGATGCCCATTCTCCAGGACTTCTCCAACTTACTATTAGACTAAACC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGCCACCCCACCAGGATGCCCATTCTCCAGGACTTCTCCAACTTACTATTAGACTAAACC  480

```
Query  481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAACAAGCAACAAACTGTATTTATGCAAGCAAAATTGATGAGAAAATTATATTCAAATA  540

Query  541  AAGCAAAAATTA  552
            ||||||||||||
Sbjct  541  AAGCAAAAATTA  552
```

# Sequence 442 matched with Sequence 101

```
Query=   Sequence ID - 442                    nt:      606
Length=606


   SEQ ID NO: 101              nt:      606

ALIGNMENTS
 Identities = 606/606 (100%), Gaps = 0/606 (0%)

Query   1    TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCaaaataaataaat   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCAAAATAAATAAAT   60

Query   61   aaataaataaataaataaataaataaaaaaataaaaaataCTTCTGCTATGAAAAACCTA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AAATAAATAAATAAATAAATAAATAAAAAAATAAAAAATACTTCTGCTATGAAAAACCTA   120

Query   121  GTTGGTATTTTTGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GTTGGTATTTTTGCTTATTTAATACTATAGAAATATGGTGATCTCATCTTTAATAGAGTG   180

Query   181  CTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACTTTAAGAATTTATAATGTTA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACTTTAAGAATTTATAATGTTA   240

Query   241  ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  ATATGAGGAAATGAAATCTGGATTATCTCACCACATATTATATAATTCATTAGTGACAGA   300

Query   301  GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTTTCCTATCTGCCTTTAAATGTTGAG   360

Query   361  ATACTACCCTTATCTCATGTGAATGGAGAAACTGCCTAAAATGCTAAAACTGACTCAGAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ATACTACCCTTATCTCATGTGAATGGAGAAACTGCCTAAAATGCTAAAACTGACTCAGAG   420

Query   421  GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GCACCCAGACATAAGTGAAGTGTGATTAGAAAATCCTGGTCAGTTGAGTCTTAGCCAAAT   480
```

```
Query  481  GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTGTACCTACTGTGTCTGCCTCTATCAAGTCAATGAAAACATGATCTGAGAACTGTAAGT  540

Query  541  CCATTTATGGAAAGGGTTGATTTANAGATATTTTGAACTTNCAGTGATGAGCCCCTTCTC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCATTTATGGAAAGGGTTGATTTANAGATATTTTGAACTTNCAGTGATGAGCCCCTTCTC  600

Query  601  AAATAG  606
            ||||||
Sbjct  601  AAATAG  606
```

# Sequence 446 matched with Sequence 102

```
Query=   Sequence ID 446
Length=341


   SEQ ID NO: 102

ALIGNMENTS
 Identities = 341/341 (100%), Gaps = 0/341 (0%)

Query  1    CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCTGTAC  60

Query  61   CAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTTCTTCATAAAG  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTTCTTCATAAAG  120

Query  121  TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCANAAATGTCACTAT  180

Query  181  TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAATATTGNACATACATTG  240

Query  241  NATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACTTCATATTTTGTACAAAATGT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  NATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACTTCATATTTTGTACAAAATGT  300

Query  301  CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCCNANAA    341
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTATGTACAGAATAAAAAAGTTCATAGAAACAGCCNANAA    341
```

Blast comparison trimmed "NANAA" from the 3' end of both sequences and reported 336 identities. The report has been manually corrected for this. "NANAA" has been appended to both sequences and identity count has been increased to 341.

# Sequence 447 matched with Sequence 103

Query=   Sequence ID 447
Length=85


    SEQ ID NO: 103

ALIGNMENTS
 Identities = 85/85 (100%), Gaps = 0/85 (0%)

```
Query  1    AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACATGGT  60

Query  61   GAAACCCCATCTCTACAAAAATATA  85
            |||||||||||||||||||||||||
Sbjct  61   GAAACCCCATCTCTACAAAAATATA  85
```

# Sequence 448 matched with Sequence 104

Query=  Sequence ID - 448                    nt:     329
Length=329


   SEQ ID NO: 104             nt:     329

ALIGNMENTS
 Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query  1    TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAG  60

Query  61   AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTG  120

Query  121  AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTTG  180

Query  181  TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTACAGAA  240

Query  241  GGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAAGATGAGTGGGAAAC  300

Query  301  CATCTCAATAAACACATTTTGGGTTAAAA   329
            |||||||||||||||||||||||||||||
Sbjct  301  CATCTCAATAAACACATTTTGGGTTAAAA   329

## Sequence 450 matched with Sequence 105

Query=   Sequence ID 450
Length=504


   SEQ ID NO: 105

ALIGNMENTS
 Identities = 504/504 (100%), Gaps = 0/504 (0%)

```
Query  1    GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATTCTCC  60

Query  61   CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTACTAAATTT  120

Query  121  GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGTCTCACTGTGATG  180

Query  181  CCCAGGCTGGTCTTGAACTCCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCAGGCTGGTCTTGAACTCCTGGGCTCAAGCAGTCACCCACCTCAGCCTCCCAAAGCAC  240

Query  241  TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTTGATGACTAAGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGTTTTGTTTTGATGACTAAGCT  300

Query  301  GCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTACCTTTCTTCTGTTTCCCTGGGCTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTACCTTTCTTCTGTTTCCCTGGGCTA  360

Query  361  GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGCTCCATGTTGGCAGTCCTACTCCCAATTAACCTGGGGCTGTCTGGTTAACCTTTATA  420

Query  421  AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGATCTGCAGTCATTGGGAGACCCGGGGACCAGGAATATTGTTGTTGAGGGAGCTACCCT  480
```

```
Query  481  GGAAAGTGGATGGGTGGCCAAAGG  504
            ||||||||||||||||||||||||
Sbjct  481  GGAAAGTGGATGGGTGGCCAAAGG  504
```

# Sequence 452 matched with Sequence 106

Query=   Sequence ID 452
Length=582


   SEQ ID NO: 106

ALIGNMENTS
 Identities = 582/582 (100%), Gaps = 0/582 (0%)

```
Query  1    TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCATTCA  60

Query  61   TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTTCTATCCAA  120

Query  121  TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAATAATTCCTGACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAATAATTCCTGACT  180

Query  181  ATGGGTTTAAAGACTGAAAATGGATCAATAGAAACTTTGAAAATGTTAACATCTTGATTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGGGTTTAAAGACTGAAAATGGATCAATAGAAACTTTGAAAATGTTAACATCTTGATTG  240

Query  241  CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAACTGCATGTTTTTAATGAGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAACTGCATGTTTTTAATGAGAT  300

Query  301  ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTTCTGGAGAAAGCCTGTTGCTATCTG  360

Query  361  CCATACCTTGGTTTACTTTGTGCAAAATGAGCTTCTTTTTAAGTAATGAGCTCTTTCCAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCATACCTTGGTTTACTTTGTGCAAAATGAGCTTCTTTTTAAGTAATGAGCTCTTTCCAT  420

Query  421  GTTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCCTGCTCTGCCTCATTCCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTCAGCTTAAATTGCTGTCTTAGACACTTCATCAGGGTTCCCTGCTCTGCCTCATTCCC  480
```

```
Query  481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCTTTTGCTCACTTGCAGCCTTTGACATAATCCTGGGAGGCAATTGGCATCATACATATT  540

Query  541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGCTTTGTAATCTCCTGCTTTGATTCTGACTGGGACCCAGC  582
```

# Sequence 453 matched with Sequence 107

Query=  Sequence ID - 453                    nt:    747
Length=747


   SEQ ID NO: 107              nt:     747

ALIGNMENTS
 Identities = 747/747 (100%), Gaps = 0/747 (0%)

```
Query   1    GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCAGTAA   60

Query   61   TAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCCAGGTCCTTGGATTTCTTTCTGT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCCAGGTCCTTGGATTTCTTTCTGT   120

Query   121  GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTAAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGGAGAAATATTAAA   180

Query   181  AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAATGTTGTTTAGGACAAG   240

Query   241  TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAAAAACCTACATAGCA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGTCATTAAAAACCTACATAGCA   300

Query   301  GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGCATGTACAAATGTCACATTCTGCCG   360

Query   361  TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TCACGTAATGGTCCTCACAGCTTGAGGTAGCATTTAGCATGTGTCATGATTTAGTACAAG   420

Query   421  GGTTGGCAAACTGTTGCTCTTGGATTAAGTCTGGCTCATTGCCTGTTTTTCAAAGaaaaa   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GGTTGGCAAACTGTTGCTCTTGGATTAAGTCTGGCTCATTGCCTGTTTTTCAAAGAAAAA   480
```

```
Query  481  aaTtgtatatgtgtgtatatatgttatatataggtacacacacatatgtgctatatatag  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATTGTATATGTGTGTATATATGTTATATATAGGTACACACACATATGTGCTATATATAG  540

Query  541  catatatacacacataatatataaacatgtacatatatagcattatatatataccgtgta  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CATATATACACACATAATATATAAACATGTACATATATAGCATTATATATATACCGTGTA  600

Query  601  taatatCTCCAGTCCTCATGACCAGCCATGCTTGTTCATTTACATTTGCATACTCTATGA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TAATATCTCCAGTCCTCATGACCAGCCATGCTTGTTCATTTACATTTGCATACTCTATGA  660

Query  661  TTGCTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC  720
            |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  661  TTGCTTTCATGCAACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCC  720

Query  721  ACTAAACCTAAAATATTAATCTCTGCC   747
            |||||||||||||||||||||||||||
Sbjct  721  ACTAAACCTAAAATATTAATCTCTGCC   747
```

# Sequence 454 matched with Sequence 108

Query=  Sequence ID 454
Length=522


   SEQ ID NO: 108

ALIGNMENTS
 Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query  1    CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCCACAG  60

Query  61   GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATGGCATATCA  120

Query  121  GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGATGAGCTCATACA  180

Query  181  GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTCAGTTTGATAAGGCTAT  240

Query  241  AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTCAGGGGCTCTCTAAATAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAATTTCAGGGGCTCTCTAAATAC  300

Query  301  GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTACAGATTCTGCGATAATGTGTGGACTTTTGTACTGAATGATGTTGAATTCAGAGAGGT  360

Query  361  GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GACAGAACTTATTAAAGTGGATAAAGTGAAAATTGTAGCCTGTGATGGTAAAAATACTGG  420

Query  421  CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTCCAATACTACAGAATGAATAGAAAAAATATGACTTTTTTACACCATCTTCTGTTATTC  480

```
Query  481  ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTTATT  522
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTGCTTTTGAAGAGAAGCATAGAAGAGACTTTTTATTTATT  522
```

# Sequence 458 matched with Sequence 109

```
Query=  Sequence ID - 458                    nt:     682
Length=682


   SEQ ID NO: 109             nt:     682

ALIGNMENTS
 Identities = 682/682 (100%), Gaps = 0/682 (0%)

Query  1    TGCCACTGAAGATCCTGGTGTCGCCATGGGCCGCCGCCCCGCCCGTTGTTACCGGTATTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCCACTGAAGATCCTGGTGTCGCCATGGGCCGCCGCCCCGCCCGTTGTTACCGGTATTG  60

Query  61   TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCCAAGATTCG  120

Query  121  CATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCTTTGTGGCCACAT  180

Query  181  GGTGTCAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGGCTGCCCGAATTTGTGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGTGTCAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGGCTGCCCGAATTTGTGC  240

Query  241  CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTCCATATCCGGGTGCGGCTCCA  300

Query  301  CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCCTGTGCTGGGGCTGACAGGCTCCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCCCTTCCACGTCATCCGCATCAACAAGATGTTGTCCTGTGCTGGGGCTGACAGGCTCCA  360

Query  361  AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AACAGGCATGCGAGGTGCCTTTGGAAAGCCCCAGGGCACTGTGGCCAGGGTTCACATTGG  420

Query  421  CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCAAGTTATCATGTCCATCCGCACCAAGCTGCAGAACAAGGAGCATGTGATTGAGGCCCT  480
```

```
Query  481  GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCGCAGGGCCAAGTTCAAGTTTCTGGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCT  540

Query  541  TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCACCAAGTTCAATGCTGATGAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCAN  600

Query  601  ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ATGGCTGTGGGGTCAAGTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCA  660

Query  661  CTCATGAAGGCTTTCAATGTGC  682
            ||||||||||||||||||||||
Sbjct  661  CTCATGAAGGCTTTCAATGTGC  682
```

# Sequence 459 matched with Sequence 110

Query=   Sequence ID 459
Length=668


   SEQ ID NO: 110

ALIGNMENTS
 Identities = 668/668 (100%), Gaps = 0/668 (0%)

```
Query  1    TCCCGGAATCGCGGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTTCCCTGAAGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCCGGAATCGCGGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTTCCCTGAAGTG  60

Query  61   GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCACATCTCTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCACATCTCTGG  120

Query  121  GCCAATTTTTGCTTGTAAGTCTTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCAATTTTTGCTTGTAAGTCTTTCCGGAGACCCCTGGAATTTAAATCATTAGCACCGCG  180

Query  181  CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGCGCAGTTCTCGCGAGAA  240

Query  241  GGTGACTTTCTTTCTCGGTATTTCCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGTGACTTTCTTTCTCGGTATTTCCTGGTTTCCAGAATCCTTAGCGCGAGGCGGAAAAAA  300

Query  301  TATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGACTGAGACTTCTTCCCACGATTTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGACTGAGACTTCTTCCCACGATTTCT  360

Query  361  GTTTTTGCTTCTCCAAGGAAAATGGCAGCTCCCGAGCAGCCGCTTGCGATATCAAGGGGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTTTTTGCTTCTCCAAGGAAAATGGCAGCTCCCGAGCAGCCGCTTGCGATATCAAGGGGA  420

Query  421  TGCACGAGCTCCTCCTCGCTTTCCCCGCCTCGGGGCGACCGAACCCTTCTGGTCAGGCAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGCACGAGCTCCTCCTCGCTTTCCCCGCCTCGGGGCGACCGAACCCTTCTGGTCAGGCAC  480
```

```
Query  481  CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTGCCGGCTGAGCTTACTGCTGAGGAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAG  540

Query  541  TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCTGTGCGGGTCCTGTCAGATAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCT  600

Query  601  AATGAAAAAGCAGCTNTAAAGGCATTGACAAACTNCATCAACTGAAACTTTTAGTCATAC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AATGAAAAAGCAGCTNTAAAGGCATTGACAAACTNCATCAACTGAAACTTTTAGTCATAC  660

Query  661  TTTAATCG  668
            ||||||||
Sbjct  661  TTTAATCG  668
```

# Sequence 460 matched with Sequence 111

Query= Sequence ID - 460          nt:     536
Length=536


   SEQ ID NO: 111         nt:    536

ALIGNMENTS
 Identities = 536/536 (100%), Gaps = 0/536 (0%)

```
Query  1    CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATTCAGG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATTCAGG   60

Query  61   TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTCTCCAAGTA   120

Query  121  CTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCTTTTCTTTCATTA   180

Query  181  AATAAATCTTTATTGAATTTCTACTACATTaaaaaaccaaaccaaaacaaaacaaacaaa   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATAAATCTTTATTGAATTTCTACTACATTAAAAAAACCAAACCAAAACAAAACAAACAAA   240

Query  241  aaaaacaCTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAAACACTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTGACTGGAACCTTGAAGGATGG   300

Query  301  GTAAACTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTAAACTTTCAGCAGATAAAGATTGAGAGAAGACCTTCCAGGTAGAGAAAGCAGTGTGGG   360

Query  361  CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CACAGGCAAAGATGGAAGAACACACGTGGCTGTGGGAAACACAGCTAGAAGCCAGTGCGG   420

Query  421  ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATAGAGAGTAGGCTATGATGTGCAAAGGTTANACACTGGGAGAGACAGGTCCATGAGAGT   480
```

```
Query  481  AGCTTGGACTAACACAGGGAGGGTTTGGAATCCCAACTGGGGAACCTANAAATCAA  536
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCTTGGACTAACACAGGGAGGGTTTGGAATCCCAACTGGGGAACCTANAAATCAA  536
```

# Sequence 461 matched with Sequence 112

```
Query=   Sequence ID 461
Length=368


   SEQ ID NO: 112

ALIGNMENTS
 Identities = 368/368 (100%), Gaps = 0/368 (0%)

Query  1    TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGC  60

Query  61   CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT  120

Query  121  TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACATG  180

Query  181  AAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTAATAATTTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTAATAATTTT  240

Query  241  CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGAAGAACCCTCCAT  300

Query  301  AAACCTGGAGTGACTATATGGATGCCCCCCACCCTACCACACATTCGAAGAACCCGTATA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAACCTGGAGTGACTATATGGATGCCCCCCACCCTACCACACATTCGAAGAACCCGTATA  360

Query  361  CATAAAAT  368
            ||||||||
Sbjct  361  CATAAAAT  368
```

## Sequence 462 matched with Sequence 113

```
Query=  Sequence ID 462
Length=338


   SEQ ID NO: 113

ALIGNMENTS
 Identities = 338/338 (100%), Gaps = 0/338 (0%)

Query  1    TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTTCTAT   60

Query  61   CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTTGCAGAATT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTTGCAGAATT   120

Query  121  TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATGTTGGTGCCAAGT   180

Query  181  ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAATGTTAATTG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGCTTGAAAATGTTAATTG   240

Query  241  CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTTGTATCTTGCTTATATTTC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATTTTGTATCTTGCTTATATTTC   300

Query  301  AGTTCCCACCTCTGTCCNGACNAAACCCCCATATATAA   338
            ||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGTTCCCACCTCTGTCCNGACNAAACCCCCATATATAA   338
```

# Sequence 463 matched with Sequence 114

```
Query=  Sequence ID 463
Length=383


   SEQ ID NO: 114

ALIGNMENTS
 Identities = 383/383 (100%), Gaps = 0/383 (0%)

Query  1    TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACTTTATA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACTTTATA  60

Query  61   GAAGTTGAGTTTTAATTAAAATTCTTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGTTGAGTTTTAATTAAAATTCTTGGCATCCTGAAGTATGTCACATAGCATGTGCTCC  120

Query  121  TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTCATTTTATAAAGTACCAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTCATTTTATAAAGTACCAT  180

Query  181  ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCTTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTTCGCTTTGCTTGNCTTT  240

Query  241  TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTTACATCATNCAACAGTTTACT  300

Query  301  TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCTATGAAAATCTTCCCATCTATATCA  360

Query  361  AAATACTTTCAAGGATATACTTT   383
            |||||||||||||||||||||||
Sbjct  361  AAATACTTTCAAGGATATACTTT   383
```

## Sequence 464 matched with Sequence 115

```
Query=  Sequence ID - 464                    nt:     615
Length=615


   SEQ ID NO: 115                 nt:     615

ALIGNMENTS
 Identities = 615/615 (100%), Gaps = 0/615 (0%)

Query  1    CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTATCTCC  60

Query  61   TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAAGAAATGGA  120

Query  121  AGCTTCTCCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCTTCTCCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCAAGATTTCCAAAA  180

Query  181  CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAAACACC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTCCCACCATTAAAACACC  240

Query  241  TGAGGCTGGAACTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGTGCTACACAGTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGAGGCTGGAACTGTTATTACAACTGCCGATGAAATTGAATTAGAAGGTGCTACACAGTG  300

Query  301  GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCACACTCTACTTCTGCTTCTGCCACCTATGGGGTCGAGGCAGGTGTGGTGCCTTGGCT  360

Query  361  AAGTCCACAGACTTCTGAGAGGCCCACGCTTTCTTCTTCTCCAGAAATAAACCCTGAAAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAGTCCACAGACTTCTGAGAGGCCCACGCTTTCTTCTTCTCCAGAAATAAACCCTGAAAC  420

Query  421  TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TCAAGCAGCTTTAATCAGAGGGCAGGATTCCACGATAGCAGCATCAGAACAGCAAGTGGC  480
```

```
Query  481  AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCGAGAATTCTTGATTCCAATGATCAGGCAACAGTAAACCCTGTGGAATTTAATACTGA  540

Query  541  GGGTGCAACACCCCATTTTCCCTTCTGGAGACTTCTAATGAAACANATTTCCTGATTGGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGGTGCAACACCCCATTTTCCCTTCTGGAGACTTCTAATGAAACANATTTCCTGATTGGC  600

Query  601  ATTAATGAANAGTCA  615
            |||||||||||||||
Sbjct  601  ATTAATGAANAGTCA  615
```

# Sequence 469 matched with Sequence 116

```
Query=   Sequence ID 469
Length=161


   SEQ ID NO: 116

ALIGNMENTS
 Identities = 161/161 (100%), Gaps = 0/161 (0%)

Query  1    GATTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAATGAT   60

Query  61   ATAATTCAAAGTGGATTaaaaaaaaaaCTGTCACCCAGAATACAATACCCAGCAAAGTTG   120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATAATTCAAAGTGGATTAAAAAAAAAACTGTCACCCAGAATACAATACCCAGCAAAGTTG   120

Query  121  TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA   161
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA   161
```

Blast comparison trimmed "NA" from the 3' end of both sequences and reported 159
identities. The report has been manually corrected for this. "NA" has been appended to
both sequences and identity count has been increased to 161.

# Sequence 471 matched with Sequence 117

```
BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.




Query=   Sequence ID 471
Length=28


   SEQ ID NO: 117                                    56.0    8e-15


ALIGNMENTS
 Identities = 28/28 (100%), Gaps = 0/28 (0%)

Query   1   TCCCGGGAATCTGCAGGATCCGTCGACT   28
            ||||||||||||||||||||||||||||
Sbjct  28   TCCCGGGAATCTGCAGGATCCGTCGACT    1
```

Blast comparison trimmed "ATCTGCAGGATCCGTCGACT" from the 3' end of the query sequence and the 5' end of the subject sequence and reported 8 identities. The report has been manually corrected for this. "ATCTGCAGGATCCGTCGACT" has been appended to the 3' end of the query sequence and 5' end of the subject sequence and identity count has been increased to 28.

## Sequence 472 matched with Sequence 118

```
Query=   Sequence ID 472
Length=258


   SEQ ID NO: 118

ALIGNMENTS
 Identities = 258/258 (100%), Gaps = 0/258 (0%)

Query  1     GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAAGTGTGAGACAGCTGCCTT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAAGTGTGAGACAGCTGCCTT   60

Query  61    GTGTGGGACTGAAAGGCAAGATTTGTTCCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTGTGGGACTGAAAGGCAAGATTTGTTCCTGCCCTTCCCTTTGTGACTTGAAGAACCCTG   120

Query  121   ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCATAATGTGAGGAG   180

Query  181   GTGGGGANACCACCCCACCCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GTGGGGANACCACCCCACCCCCATGTCCACCATGACCCTCTTNCCACNCTNACCTGTGCT   240

Query  241   CCCTCCCCAATCATNTTT   258
             ||||||||||||||||||
Sbjct  241   CCCTCCCCAATCATNTTT   258
```

# Sequence 473 matched with Sequence 119

```
Query=  Sequence ID - 473                    nt:      694
Length=694


   SEQ ID NO: 119                 nt:      694

ALIGNMENTS
 Identities = 694/694 (100%), Gaps = 0/694 (0%)

Query  1    TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTTAAGA  60

Query  61   TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGAGGCCTCGG  120
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  61   TGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGAGGCCTCGG  120

Query  121  CCAATCTGGGCGGCGTGCCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAATCTGGGCGGCGTGCCCAGCAAGAGATTAAAGATGCAGTACGCCACGGGGCCGCTGC  180

Query  181  TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTTGAGGAGTACATGCGGG  240

Query  241  TTATTAGCCAGCGGTACCCAGACACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTATTAGCCAGCGGTACCCAGACACATCCGCATTGAAGGAGAGAATTACCTCCCTCAACCAA  300

Query  301  TATATAGACACATAGCATCTTTCCTGTCAGTCTTCAAACTAGTATTAATAGGCTTAATAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATATAGACACATAGCATCTTTCCTGTCAGTCTTCAAACTAGTATTAATAGGCTTAATAA  360

Query  361  TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTGTTGGCAAGGATCCTTTTGCTTTCTTTGGCATGCAAGCTCCTAGCATCTGGCAGTGGG  420

Query  421  GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCCAAGAAAATAAGGTTTATGCATGTATGATGGTTTTCTTCTTGAGCAACATGATTGAGA  480
```

```
Query   481   ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   ACCAGTGTATGTCAACAGGTGCATTTGAGATAACTTTAAATGATGTACCTGTGTGGTCTA   540

Query   541   AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACTTGTTCAAATTCTTGACAATGAAA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   AGCTGGAATCTGGTCACCTTCCATCCATGCAACAACTTGTTCAAATTCTTGACAATGAAA   600

Query   601   TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   TGAAACTCAATGTGCATATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAG   660

Query   661   CACTGNAAACTCTTTTGCATTAAGGGATCATTGC   694
              |||||||||||||||||||||||||||||||||
Sbjct   661   CACTGNAAACTCTTTTGCATTAAGGGATCATTGC   694
```

# Sequence 474 matched with Sequence 120

```
Query=   Sequence ID 474
Length=337


   SEQ ID NO: 120

ALIGNMENTS
 Identities = 337/337 (100%), Gaps = 0/337 (0%)

Query  1    GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCAATCG  60

Query  61   GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAACTGTCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGTAACTGTCA  120

Query  121  GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCTACGGGCttgttgctgttgatgttttg  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCTACGGGCTTGTTGCTGTTGATGTTTTG  180

Query  181  ttttgttttgttttttggtctttttttgTATTATAAAAAATAATCTATTTCTATGAGAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTTGTTTTGTTTTTTGGTCTTTTTTTGTATTATAAAAAATAATCTATTTCTATGAGAAA  240

Query  241  AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACACTTTTAATA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAGCATTAAGAACACTTTTAATA  300

Query  301  AACtttttttttGATAATGGTTaaaaaaaaaaaaaaaaa  337
            |||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACTTTTTTTTGATAATGGTTAAAAAAAAAAAAAAAAA  337
```

# Sequence 475 matched with Sequence 121

Query=   Sequence ID 475
Length=210


   SEQ ID NO: 121

ALIGNMENTS
 Identities = 210/210 (100%), Gaps = 0/210 (0%)

```
Query  1    CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAAACTTCCTCAGCATGGTGAAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAAACTTCCTCAGCATGGTGAAGG  60

Query  61   CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAAAGCTTTTC  120

Query  121  TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTATTCAACTCATTAT  180

Query  181  TGGAAGTTTTTGCCAGAGCAATTAGGTAAG   210
            ||||||||||||||||||||||||||||||
Sbjct  181  TGGAAGTTTTTGCCAGAGCAATTAGGTAAG   210
```

# Sequence 476 matched with Sequence 122

```
Query=   Sequence ID - 476                    nt:      476
Length=476


   SEQ ID NO: 122                  nt:     476

ALIGNMENTS
 Identities = 476/476 (100%), Gaps = 0/476 (0%)

Query  1    CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTGGCTA  60

Query  61   ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAAGATCTTAG  120

Query  121  GCCATTCACAACTCTTTTGTAAAAATTAATGTGGATGTGAAACGAGGCAACAAATCCTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCATTCACAACTCTTTTGTAAAAATTAATGTGGATGTGAAACGAGGCAACAAATCCTGA  180

Query  181  AGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTAATCCTGGCACTTTGGG  240

Query  241  AGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGACCATCCTGGCCAACATGATGA  300

Query  301  AACCCCATCTCTACTAAAATACAAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACCCCATCTCTACTAAAATACAAAAAATTAGCTGGGCATGGTGACGCGTGCCTGTAGTC  360

Query  361  CCAGTTACTCGGGAGGCTGAGGCAGGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCAGTTACTCGGGAGGCTGAGGCAGGGGAATTGCTTGAACCTCGGAGGTGGGAGGTTGCA  420

Query  421  GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT    476
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGTGCCGAGATCACGCTACTGCACTCCAGCCTGGCAACAGAGCAAGACTCCATCT    476
```

# Sequence 477 matched with Sequence 123

```
Query=   Sequence ID 477
Length=250


   SEQ ID NO: 123

ALIGNMENTS
 Identities = 250/250 (100%), Gaps = 0/250 (0%)

Query  1    AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAAAAAT  60

Query  61   TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGATCACGAGG  120

Query  121  TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTACGAAAAATACCA  180

Query  181  AAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG  240

Query  241  CAGGAGAATG  250
            ||||||||||
Sbjct  241  CAGGAGAATG  250
```

# Sequence 478 matched with Sequence 124

```
Query=   Sequence ID 478
Length=523
```

```
   SEQ ID NO: 124
```

```
ALIGNMENTS
 Identities = 523/523 (100%), Gaps = 0/523 (0%)
```

```
Query  1     TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGATTGTG  60

Query  61    TGGTCTTTGAGGGGGGTGttttttttAAGACAACATTGACCACTGTCCACTGTCCACATGA  120
             ||||||||||||||||||| |||||| |||||||||||||||||||||||||||||||||
Sbjct  61    TGGTCTTTGAGGGGGGGTGTTTTTTTTAAGACAACATTGACCACTGTCCACTGTCCACATGA  120

Query  121   TCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATAATTCCAGTGATT  180

Query  181   GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGGCATCTTTGAGCAGAGC  240

Query  241   CTGGCTATGCAGCATCATTTGAGTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG  300
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  241   CTGGCTATGCAGCATCATTTGAGTTTTTTAAACACCCTANAGGTCTGGTTGTTGTTGCTG  300

Query  301   TTGTCCTTTCCTGTGAAAGTCACCaananaaGTTACAGTCCAGGTGAACCTGGAGTTTATA  360
             ||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Sbjct  301   TTGTCCTTTCCTGTGAAAGTCACCAANANAAGTTACAGTCCAGGTGAACCTGGAGTTTATA  360

Query  361   GGTTGGTTTTGTTTCTGntatatatatatatatatatattttttttttttttttAACATTT  420
             |||||||||||||||| |||||||||||||||||||||| |||||||||||||||||||||
Sbjct  361   GGTTGGTTTTGTTTCTGNTATATATATATATATATATATATTTTTTTTTTTTTTTTTAACATTT  420

Query  421   ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ACCTGTAGTGCTGTAGCTGTTGATACTATCACCTGCATGCTATTTCTAGTGAGTGCTAAA  480
```

```
Query  481  TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG  523
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TACAGTATGGTCCAATGACAATAACAGCCCATGGTACTGCCAG  523
```

# Sequence 479 matched with Sequence 125

Query=  Sequence ID 479
Length=487


   SEQ ID NO: 125

ALIGNMENTS
 Identities = 487/487 (100%), Gaps = 0/487 (0%)

```
Query  1    CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATATCTTT  60

Query  61   CCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAGGCTTGAAA  120

Query  121  GAGCTTTCAGAATATGTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGCTTTCAGAATATGTTCGGAATCAGCAAACCATCGGAGCTCGTAAGGAGCTCCAGAAA  180

Query  181  GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATATAATTTTATATGTCAAG  240

Query  241  GAGGAGATGaaaaaaaaCAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGGAGATGAAAAAAAAACAACATCCCAGAGCCAGTTGTCATCGGAATAGTCTGGTCAAGT  300

Query  301  GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAGCTTGTAGCAGAGCAAGCCATCAAG  360

Query  361  CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CACTTGAAGCAATACAGCCCTCTACTTGCTGCCTTTACTACTCAAGGTCAGTCTGAGCTG  420

Query  421  ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTCATGAAAGCCTTC  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACTCTGTTACTGAAGATTAGGGAGTATTGCTATGACAACATTCATTTCATGAAAGCCTTC  480
```

```
Query  481  CANAAAA  487
            |||||||
Sbjct  481  CANAAAA  487
```

# Sequence 481 matched with Sequence 126

```
Query=   Sequence ID 481
Length=274


   SEQ ID NO: 126

ALIGNMENTS
 Identities = 274/274 (100%), Gaps = 0/274 (0%)

Query  1    CACACTTTCATGATAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACACTTTCATGATAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAATAAA  60

Query  61   GACCATATATGAGAAGCCCACAGCTAACATACTGTATGGTGAAAAACTGAAAGCTCTTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GACCATATATGAGAAGCCCACAGCTAACATACTGTATGGTGAAAAACTGAAAGCTCTTCC  120

Query  121  TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATCGAACGTAGTACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATCGAACGTAGTACT  180

Query  181  GGAAGCCCTAGCCAGAACAACTAGGCAATAGAAAGAAATTAAAGGCATCCATNTCAGAAA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  181  GGAAGCCCTAGCCAGAACAACTAGGCAATAGAAAGAAATTAAAGGCATCCATNTCAGAAA  240

Query  241  GGAAGAANCAAAATGCTGTCTGTTTAANATGACA   274
            |||||||||||||||||||||||||||||||||
Sbjct  241  GGAAGAANCAAAATGCTGTCTGTTTAANATGACA   274
```

## Sequence 482 matched with Sequence 127

Length=130
 Identities = 130/130 (100%), Gaps = 0/130 (0%)

```
Query  1    TTTCTATanaaaaaaattttttaaaataattgtaaagttagatttaaaattgtaaaatat  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTCTATANAAAAAAATTTTTTAAAATAATTGTAAAGTTAGATTTAAAATTGTAAAATAT  60

Query  61   aaaatcacaaaggaatgtacccaataaaatgtaaatgcnccataaaaaaaaaaaaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAATCACAAAGGAATGTACCCAATAAAATGTAAATGCNCCATAAAAAAAAAAAAAAAAA  120

Query  121  aaaaaaaaaa  130
            ||||||||||
Sbjct  121  AAAAAAAAAA  130
```

## Sequence 483 matched with Sequence 128

Query=  Sequence ID 483
Length=519


   SEQ ID NO: 128

ALIGNMENTS
 Identities = 519/519 (100%), Gaps = 0/519 (0%)

```
Query  1    CGNTAACGTGCAATCCGCCGCACGCCAGCAAACTGGACAAACTCCGGGATCTCATCGAAGCGA  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGNTAACGTGCAATCCGCCGCACGCCAGCAAACTGGACAAACTCCGGGATCTCATCGAAGCGA  63

Query  64   TTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   TTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTCGCTCATCCAGC  123

Query  124  TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG  183
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  124  TTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAGAATCAACAAGTCAGG  183

Query  184  CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAAGGTATTT  243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184  CTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCTCGCCAGTGGAAAGGTATTT  243

Query  244  AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG  303
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  AAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGCTGCGCCAGTTGCATGCAACGCGG  303

Query  304  TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC  363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  TGCATCCTTTACTTCATCCTGAATGATCTCAGCCGTAGTGCGTCCGGTGCCATCTTCGCC  363

Query  364  AGGGCCGAGCATATCGGTGTTATTCCGCTGCCATTCGTCGCTGACGAGTTTTTGCAATTG  423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364  AGGGCCGAGCATATCGGTGTTATTCCGCTGCCATTCGTCGCTGACGAGTTTTTGCAATTG  423

Query  424  CTCGAAGGAGAGACGAGTGATGTGGGAAAACTGGCTTTGCCGTTCACCTTTCAAAAGCGG  483
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  424  CTCGAAGGAGAGACGAGTGATGTGGGAAAACTGGCTTTGCCGTTCACCTTTCAAAAGCGG  483
```

```
Query  484  GAAGTTCCCCCGCCAGCGCGCGGGCCAGGGCCCGAT  519
            ||||||||||||||||||||||||||||||||||||
Sbjct  484  GAAGTTCCCCCGCCAGCGCGCGGGCCAGGGCCCGAT  519
```

Blast comparison trimmed "CGN" from the 5' end of both sequences and reported 516 identities. The report has been manually corrected for this. "CGN" has been prepended to both sequences and identity count has been increased to 519.

# Sequence 484 matched with Sequence 129

Query=   Sequence ID 484
Length=272


    SEQ ID NO: 129

ALIGNMENTS
 Identities = 272/272 (100%), Gaps = 0/272 (0%)

```
Query  1    tttttttttttttATTCTattaaaaaatgttnntgaaaaaagatacttaaattttaaagat  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTTTTTATTCTATTAAAAAATGTTNNTGAAAAAAGATACTTAAATTTTAAAGAT  60

Query  61   aactnaattcctaangatttaaaatAATCCAAGCAGAGATGAAAGANCAAATGCAAATGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACTNAATTCCTAANGATTTAAAATAATCCAAGCAGAGATGAAAGANCAAATGCAAATGC  120

Query  121  NTAAAAAGACCCCANAGCATTGTTagcaaaaagcaaatatagttagccaagcatatatat  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  NTAAAAAGACCCCANAGCATTGTTAGCAAAAAGCAAATATAGTTAGCCAAGCATATATAT  180

Query  181  ntcataaaagcaataanaaggcntaaagcaagTTTGGGGAGAGCTTATTTAAAACTTGTA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  NTCATAAAAGCAATAANAAGGCNTAAAGCAAGTTTGGGGAGAGCTTATTTAAAACTTGTA  240

Query  241  AAAATCATTTGAATTTTTAAAAGTTTTCAAAC  272
            ||||||||||||||||||||||||||||||||
Sbjct  241  AAAATCATTTGAATTTTTAAAAGTTTTCAAAC  272
```

# Sequence 485 matched with Sequence 130

```
Query=   Sequence ID - 485                    nt:      551
Length=551


   SEQ ID NO: 130                  nt:     551

ALIGNMENTS
 Identities = 551/551 (100%), Gaps = 0/551 (0%)

Query  1     TTTGGAACACAAAGTTCCCTTTTTAGAAGAATAGGTATTGAGCCCTTGAGCGTGGGTAGA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTTGGAACACAAAGTTCCCTTTTTAGAAGAATAGGTATTGAGCCCTTGAGCGTGGGTAGA  60

Query  61    AAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATGAATTTTCA  120

Query  121   CTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAAAGTNTNTTAATG  180
             ||||||||||||||||||||||||| |||| |||||||||||||||||||| | ||||||
Sbjct  121   CTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAAAGTNTNTTAATG  180

Query  181   AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTAATAAGGATGTAATAGT  240

Query  241   TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCAGAAAAGAATTAGAACAAATA  300

Query  301   ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCttttatattttatattttatttttC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCTTTTATATTTTATATTTTATTTTTC  360

Query  361   TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA  420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TCTCTTCANATGAGCATTCTCTTTCTATGTCCATATGGTANAAGGCGGCAGCTCCATAGA  420

Query  421   TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTCAGTC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TTATGGCTTCAGATGTTACAGTTCCGCTNAATGCAGGGACAGACTTGCTATCTTTCAGTC  480
```

```
Query  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCCGTTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCTTACATATCCTGGGGAGAGAGCAAATGATTGACTGGCTTGAGTCAGGTGCCCGTTCC  540

Query  541  CTTTCCAATCT  551
            |||||||||||
Sbjct  541  CTTTCCAATCT  551
```

# Sequence 487 matched with Sequence 131

```
Query=   Sequence ID - 487 nt:224
Length=224


   SEQ ID NO: 131 nt:224

ALIGNMENTS
 Identities = 224/224 (100%), Gaps = 0/224 (0%)

Query  1    GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAATATGT  60

Query  61   TCTTAGAAGCANGAAAAAGAATTCAGNTTTGCTTTGTATACTAAATTAAATGCTGTAATT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTTAGAAGCANGAAAAAGAATTCAGNTTTGCTTTGTATACTAAATTAAATGCTGTAATT  120

Query  121  TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCTTGACGTCAGCCT  180

Query  181  CACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC  224
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC  224
```

# Sequence 488 matched with Sequence 132

```
Query=  Sequence ID - 488                    nt:    349
Length=349


   SEQ ID NO: 132                 nt:    349

ALIGNMENTS
 Identities = 349/349 (100%), Gaps = 0/349 (0%)

Query  1    GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTAtttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTATTTT  60

Query  61   tttGTATTAGATAGCATTAACCTTACTGTTGAAGTATTTTTGGTGGAGTATTAGTGACAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTGTATTAGATAGCATTAACCTTACTGTTGAAGTATTTTTGGTGGAGTATTAGTGACAA  120

Query  121  GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTTCGTGTGTGTTTGTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTTCGTGTGTGTTTGTG  180

Query  181  TGTAGGTTACGTTATATATAGGATTCGTGTTCGCCGTGGTGGCCGAAAACGCCCAGTTCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTAGGTTACGTTATATATAGGATTCGTGTTCGCCGTGGTGGCCGAAAACGCCCAGTTCC  240

Query  241  TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTTAACCAGCTAAAGTTTGCTCG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTTAACCAGCTAAAGTTTGCTCG  300

Query  301  AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC   349
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACNCCCTGGGGGGCTC   349
```

# Sequence 489 matched with Sequence 133

Query=  Sequence ID 489
Length=635


   SEQ ID NO: 133

ALIGNMENTS
 Identities = 635/635 (100%), Gaps = 0/635 (0%)

```
Query   1    TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCAGACAAGTAAAATATCTG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCAGACAAGTAAAATATCTG   60

Query   61   TTTTTCACGCaaaaaaaGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TTTTTCACGCAAAAAAAGCCATGAAATACGTAATTTTTTAAAGACAAAAAATCATCTTTT   120

Query   121  GAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAACAGAAAGATTCTT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAACAGAAAGATTCTT   180

Query   181  TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTACCAGGAAGAAAGAGGAT   240

Query   241  TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTTAATGTGGTTGC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGGTTTTGTTTTAATGTGGTTGC   300

Query   301  CCTGTCCACTACATGGTTCTATCAGTAGTGTAATCCATTTTCAATGTAAAGCTCTTTTAG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  CCTGTCCACTACATGGTTCTATCAGTAGTGTAATCCATTTTCAATGTAAAGCTCTTTTAG   360

Query   361  TTTTTGTCATAGACATAAATTAATATTTTGAGAGGCATCCCTCACCTGTTCATTTCTTCT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TTTTTGTCATAGACATAAATTAATATTTTGAGAGGCATCCCTCACCTGTTCATTTCTTCT   420

Query   421  GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GTGTTGAAATGAAGTACTTAAAATTACCGTTATACATGAACTTTGTGGACTGTAAGATTT   480
```

```
Query  481  GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTTAATTAATATGCCTGTTTTGAGTGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTATATATGTTCAAATGCCTTTTAGCTGGCTTTTTAATTAATATGCCTGTTTTGAGTGC  540

Query  541  TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTAATACAATGTAATGNGGATTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATA  600

Query  601  TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC  635
            |||||||||||||||||||||||||||||||||||
Sbjct  601  TTTGNACTCAGAGAGCCTTATTTTATTCTTCCAGC  635
```

# Sequence 491 matched with Sequence 134

```
Query=  Sequence ID - 491                    nt:      382
Length=382


   SEQ ID NO: 134                 nt:      382

ALIGNMENTS
 Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query  1    TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA  60

Query  61   CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA  120

Query  121  ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG  180

Query  181  CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG  240

Query  241  AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC  300

Query  301  CATCTCaaaaaaaaaaaaaaaaaaaCAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATCTCAAAAAAAAAAAAAAAAAAACAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT  360

Query  361  AGTTTGTAGAAACATTAAAAGT   382
            ||||||||||||||||||||||
Sbjct  361  AGTTTGTAGAAACATTAAAAGT   382
```

# Sequence 492 matched with Sequence 135

```
Query=   Sequence ID 492
Length=503


   SEQ ID NO: 135

ALIGNMENTS
 Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query  1    ACCCTAAACATAACTTAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCCTAAACATAACTTAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTAATTG  60

Query  61   AGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATATCTGTAAGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATATCTGTAAGT  120

Query  121  TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCCACCCTGGGAATC  180

Query  181  TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGTCTGGTTTAGAAATCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGTCTGGTTTAGAAATCTG  240

Query  241  ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTGGAAGATACGATTTTGTTATC  300

Query  301  AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACTCCTTATTAATATATTTAAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAGNATGTTTCTGTTTTATAGATTTTATTCATCTACAACTCCTTATTAATATATTTAAG  360

Query  361  AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANCGGTGGTAAAAGGTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAGTCATTAACCCACCATTGATTACTTGATATAAAAGGAGAANCGGTGGTAAAAGGTGAA  420

Query  421  ATANAAtttttaatttttttttttttaagtttaggatttttttttAAATTCTAAGAGTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATANAATTTTTAATTTTTTTTTTTTTTAAGTTTAGGATTTTTTTTTAAATTCTAAGAGTTT  480
```

```
Query  481  CTGTCATTTGGGGACAATCAGAA  503
            |||||||||||||||||||||||
Sbjct  481  CTGTCATTTGGGGACAATCAGAA  503
```

# Sequence 493 matched with Sequence 136

Query=   Sequence ID 493
Length=576


    SEQ ID NO: 136

ALIGNMENTS
 Identities = 576/576 (100%), Gaps = 0/576 (0%)

```
Query   1    TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAAGAAC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAAGAAC   60

Query   61   GGAAAGATTGAATATCAGTTTCCCTTCTTTaaaaaaaTTGTGGATATGTGATCTAGCTTC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GGAAAGATTGAATATCAGTTTCCCTTCTTTAAAAAAATTGTGGATATGTGATCTAGCTTC   120

Query   121  TTGAGCATCACAGTGACTGATTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TTGAGCATCACAGTGACTGATTGGCTCGTGGTAATTGATCGCTATGCTGACAATCTTATC   180

Query   181  TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATCAGGAGGAGAGTTTAGC   240

Query   241  TCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCCCAACTTGTGGAAACAGCTAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCCCAACTTGTGGAAACAGCTAA   300

Query   301  AGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAAAATGTAGCAACATGTGTTTCCTGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAAAATGTAGCAACATGTGTTTCCTGA   360

Query   361  AACAAAATTCCACTATAATAaaaaaaaaGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AACAAAATTCCACTATAATAAAAAAAAGCATTTGAATGCTCCCTTGTAATTCTGTTGGAGC   420

Query   421  TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TTGTTGCCTTTTTTATGACACAACCATAATCAGTGATAGACAGTAGCATAAAGAAGCAAG   480
```

```
Query   481   AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AGCAAAGCAATTAAGTAATAATAGCACTACAAAAATGTGTGCTGTACTTACCAAACACGA   540

Query   541   CATTTATGAATTATTANATAGGAATAAGGGGATGGT   576
              ||||||||||||||||||||||||||||||||||||
Sbjct   541   CATTTATGAATTATTANATAGGAATAAGGGGATGGT   576
```

# Sequence 494 matched with Sequence 137

```
BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.




Query=   Sequence ID 494
Length=22


   SEQ ID NO: 137                                     44.1    2e-11

ALIGNMENTS
 Identities = 22/22 (100%), Gaps = 0/22 (0%)

Query  1    GACCCAGCCATCTAAATAAGTT  22
            ||||||||||||||||||||||
Sbjct  1    GACCCAGCCATCTAAATAAGTT  22
```

## Sequence 495 matched with Sequence 138

```
Query  1    TTTC
            ||||
Sbjct  1    TTTC
```

# Sequence 496 matched with Sequence 139

```
Query=   Sequence ID 496
Length=431


   SEQ ID NO: 139

ALIGNMENTS
 Identities = 431/431 (100%), Gaps = 0/431 (0%)

Query  1    CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGGATGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGGATGG  60

Query  61   TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGTGCGCGACC  120

Query  121  GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAATCGCTGACTTAC  180

Query  181  CTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAGATTGTATGTGATTTAT  240

Query  241  AAAGTTCCGCAAGTCATAGTACTGGATTTCCAGAAAGTGAAACTAAAATTTTAATCCAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAGTTCCGCAAGTCATAGTACTGGATTTCCAGAAAGTGAAACTAAAATTTTAATCCAGG  300

Query  301  TGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCCATCTCCAGGGGATGTAAAAGCAAT  360

Query  361  CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAAGAATGCCATAGCAAATGCTTNAACTCTGGCTGAAGTGGANAGGCTGAANGGGTTGCT  420

Query  421  GCAGTCTGGTC    431
            |||||||||||
Sbjct  421  GCAGTCTGGTC    431
```

## Sequence 497 matched with Sequence 140

Query=   Sequence ID 497
Length=606


   SEQ ID NO: 140

ALIGNMENTS
 Identities = 606/606 (100%), Gaps = 0/606 (0%)

```
Query  1    GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGTTTG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTGTTTG   60

Query  61   TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGGCACAGAAG   120

Query  121  AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACGCTTTATGANAAG   180

Query  181  TGACCACCTTGCCAAACATATTAAAACACACCAGAATAAAAAAGGTATTCACTCTANCAG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGACCACCTTGCCAAACATATTAAAACACACCAGAATAAAAAAGGTATTCACTCTANCAG   240

Query  241  TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACTTTGATTACTGCAGGAGGAAC   300

Query  301  AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACGCTTATCCTTGCAAATATTCAACAAGGTTCTGTTTCAGGGATAGGAACTGTTAATAC   360

Query  361  TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTCAC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCCGCCACCAGCAATCAAGATATCCTTACCAACACTGAAATACCTTTACAGCTTGTCAC   420

Query  421  AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGTTA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTTTCTGGAAATGAGACAATGGGAGTAAATATTACACAAATACTTATTCATTGNGGTTA   480
```

```
Query  481  TTTTTATACAGTAGTGAGAAGAATATTGTTCCTAAGTTCTTAGATATCttttttttGGATG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTTTATACAGTAGTGAGAAGAATATTGTTCCTAAGTTCTTAGATATCTTTTTTTGGATG  540

Query  541  TGCAAAAATTTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCAAAAATTTTTGGATTGACAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTT  600

Query  601  GGATGA  606
            ||||||
Sbjct  601  GGATGA  606
```

# Sequence 499 matched with Sequence 141

Query=  Sequence ID 499
Length=564


   SEQ ID NO: 141

ALIGNMENTS
 Identities = 564/564 (100%), Gaps = 0/564 (0%)

```
Query  1    TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTCATCCAGTCAGCCAACCAGCCCTCCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTCATCCAGTCAGCCAACCAGCCCTCCG  60

Query  61   ANGGGCAGGCCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCCAAGGACAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ANGGGCAGGCCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCCAAGGACAC  120

Query  121  CCAACACAATTTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTCCTCCCCANAGGAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAACACAATTTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTCCTCCCCANAGGAC  180

Query  181  CCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCACTACACCCCATGCCTGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCACTACACCCCATGCCTGG  240

Query  241  GGGCCGAGATTCTCCAGCAGAAAGATGCAATAtttttttgtttcctttttttccatttttt  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGGCCGAGATTCTCCAGCAGAAAGATGCAATATTTTTTGTTTCCTTTTTTTCCATTTTTT  300

Query  301  tCTCTAAGGAATCAATATTTCAATATGTTGAGTGTGTGTCCAATGCTATGAAATTAAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCTCTAAGGAATCAATATTTCAATATGTTGAGTGTGTGTCCAATGCTATGAAATTAAAAT  360

Query  361  ATTAAATAACATATTTATGGCATTTTCTTGAAGAGTGTGGTTGAAGAAATATTTCTCCtt  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTAAATAACATATTTATGGCATTTTCTTGAAGAGTGTGGTTGAAGAAATATTTCTCCTT  420

Query  421  ttgtttttctttttttttttGNTTGNTACTGCCACTTCTTTTTAGGAGCAAATCTCCCCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTGTTTTTCTTTTTTTTTTTGNTTGNTACTGCCACTTCTTTTTAGGAGCAAATCTCCCCAG  480
```

```
Query  481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGTGTACGGNATTTCTTGACTCTGGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGT  540

Query  541  TCTGCCCTCAAATGGAATTAAGTG  564
            ||||||||||||||||||||||||
Sbjct  541  TCTGCCCTCAAATGGAATTAAGTG  564
```

# Sequence 500 matched with Sequence 142

```
Query=   Sequence ID - 500                    nt:      390
Length=390


   SEQ ID NO: 142                 nt:      390

ALIGNMENTS
 Identities = 390/390 (100%), Gaps = 0/390 (0%)

Query  1     GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAAGCTA   60

Query  61    TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCAGCACATCA   120

Query  121   TTAGGCTTTATGACTGGgtgtgtgttgtgtgtatgtaatacataatgtttattgtacana  180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TTAGGCTTTATGACTGGGTGTGTGTTGTGTGTATGTAATACATAATGTTTATTGTACANA  180

Query  181   tgtgtggggtttgtgttttATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT  240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGTGTGGGGTTTGTGTTTTATGATACATTACAGCCAAATTATTTGTTGGTTNATGGACAT  240

Query  241   ACTGCCCTTTCAtttttttCTTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACTGCCCTTTCATTTTTTTCTTTTCCAGTGTTTAGGTGATCTCAAATTAAGAAATGCATT  300

Query  301   TAACCATGTAAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAACCATGTAAAANATGANTGCTAAAGTCAGCTTTTTAGGGCCCTTTGCCAATAGGTANT  360

Query  361   CATTCAATCTGGTATTGATCTTTTCACAA   390
             |||||||||||||||||||||||||||||
Sbjct  361   CATTCAATCTGGTATTGATCTTTTCACAA   390
```

# Sequence 502 matched with Sequence 143

Query=   Sequence ID 502
Length=546


   SEQ ID NO: 143

ALIGNMENTS
 Identities = 546/546 (100%), Gaps = 0/546 (0%)

```
Query  1    ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAGGCAC  60

Query  61   CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCCTTTGGCCACATATAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCCTTTGGCCACATATAT  120

Query  121  GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTACTGTTCAAAAAGG  180

Query  181  AATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACAATGTTACCCAGCATGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACAATGTTACCCAGCATGC  240

Query  241  TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATTCTTGCCAAGAGAATTAATGT  300

Query  301  GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGATAGCTTCCTGAAACGTGTGAAGGA  360

Query  361  AAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAATGATCAGAAAAAGAAAGAAGCCAAAGAGAAAGGTACCTGGGTTCAACTAAAGCGCCA  420

Query  421  GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCCTGCTCCACCCAGAGAAGCACACTTTGTGAGAACCAATGGGAAGGAGCCTGAGCTGCT  480
```

```
Query  481  GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTaaaaaaaaaaaaTAAAGGACC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGAACCTATTCCCTATGAATTCATGGCATAATAGGTGTTAAAAAAAAAAAAATAAAGGACC  540

Query  541  TCTGGG  546
            ||||||
Sbjct  541  TCTGGG  546
```

# Sequence 503 matched with Sequence 144

```
Query=   Sequence ID - 503                  nt:     109
Length=109


   SEQ ID NO: 144               nt:     109

ALIGNMENTS
 Identities = 109/109 (100%), Gaps = 0/109 (0%)

Query  1    ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCACCAC  60

Query  61   TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC  109
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC  109
```

# Sequence 504 matched with Sequence 145

```
Query=   Sequence ID - 504                    nt:      374
Length=374


   SEQ ID NO: 145                  nt:      374

ALIGNMENTS
 Identities = 374/374 (100%), Gaps = 0/374 (0%)

Query  1    CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCTGGCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCTGGCG  60

Query  61   CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAAAGAAGCTA  120

Query  121  CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTTCCCTTAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTTATTTTCCCTTAA  180

Query  181  ATTATTTTTGTAATGGTAGCTTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTATTTTTGTAATGGTAGCTTTTTCTACATCTTACTCCTGTTGATGCAGCTAAGGTACA  240

Query  241  TTTGTaaaaagaaaaaaaaCCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTGTAAAAAGAAAAAAAACCAGACTTTTCANACAAACCCTTTGTATTGTANATAAGAGG  300

Query  301  AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTTACAGTATTTGTAAGAATAAAGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAAGACTGAGCATGCTCACTTTTTTATATTAATTTTTACAGTATTTGTAAGAATAAAGC  360

Query  361  ANCATTTGAAATCG  374
            ||||||||||||||
Sbjct  361  ANCATTTGAAATCG  374
```

# Sequence 505 matched with Sequence 146

```
Query=  Sequence ID 505
Length=357


   SEQ ID NO: 146

ALIGNMENTS
 Identities = 357/357 (100%), Gaps = 0/357 (0%)

Query  1    GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTATTTG  60

Query  61   GAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATAGTCTTGTT  120

Query  121  CTCACAGACAACAGATGGCCATCATCTTAAAACAACATTTATGTTAACCAGCAGATAAGG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCACAGACAACAGATGGCCATCATCTTAAAACAACATTTATGTTAACCAGCAGATAAGG  180

Query  181  GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACTTGCATAGGTGAAAGTG  240

Query  241  GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTACCCCTTAGGGAGCTCCAGTTT  300

Query  301  GCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTTCCTGAGGACAGCCCGACTTCT  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTTCCTGAGGACAGCCCGACTTCT  357
```

# Sequence 506 matched with Sequence 147

```
Query=  Sequence ID 506
Length=293


   SEQ ID NO: 147

ALIGNMENTS
 Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query  1    GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCTGAGG  60

Query  61   TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGAGGATGGAG  120

Query  121  CTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTAACGCACAACTTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTAACGCACAACTTG  180

Query  181  CTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGTAAAATGGAATTTTGACTGATTTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGTAAAATGGAATTTTGACTGATTTG  240

Query  241  TTACAATAATATAACTCTGAGATGTGTGaaaaaaaaaaaaaaaaaaaaaaaa   293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTACAATAATATAACTCTGAGATGTGTGAAAAAAAAAAAAAAAAAAAAAAAA   293
```

## Sequence 507 matched with Sequence 148

```
Query=   Sequence ID - 507                    nt:     521
Length=521


   SEQ ID NO: 148                 nt:     521

ALIGNMENTS
 Identities = 521/521 (100%), Gaps = 0/521 (0%)

Query  1    CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCAT  60

Query  61   CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAA  120

Query  121  GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGG  180

Query  181  ACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACT  240

Query  241  TCGTGGTGGTGCTaagaaaaggaagaagaagtcttacaccactcccaagaagaataagca  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCA  300

Query  301  caagagaaagaagGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAA  360

Query  361  AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGC  420

Query  421  AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACC  480
```

```
Query  481  AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT  521
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT  521
```

## Sequence 508 matched with Sequence 149

Query= Sequence ID 508
Length=470


   SEQ ID NO: 149

ALIGNMENTS
 Identities = 470/470 (100%), Gaps = 0/470 (0%)

```
Query  1    AAGCTCATGATTTTAAATGTATTTTTCTAATAAACTATACTCCCATTTAAAAATCACCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAGCTCATGATTTTAAATGTATTTTTCTAATAAACTATACTCCCATTTAAAAATCACCAA  60

Query  61   TACCTTAATGTTTCAATTATATAAGCTAATTAAAAATAAAGGCTGGGCGTGGTGGCTCAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TACCTTAATGTTTCAATTATATAAGCTAATTAAAAATAAAGGCTGGGCGTGGTGGCTCAC  120

Query  121  TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAA  180

Query  181  CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCC  240

Query  241  CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGG  300

Query  301  GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAACTCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAACTCC  360

Query  361  ATCTCaaaaataataaaaaaaataaaataaaaataaaattcaaacctaaaataGATGCTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCTCAAAAATAATAAAAAAAATAAAATAAAAATAAAATTCAAACCTAAAATAGATGCTC  420

Query  421  TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCtttttttGGGCTTTC     470
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTTTTTTTGGGCTTTC     470
```

## Sequence 509 matched with Sequence 150

```
Query=   Sequence ID - 509                    nt:     575
Length=575


   SEQ ID NO: 150                  nt:     575

ALIGNMENTS
 Identities = 575/575 (100%), Gaps = 0/575 (0%)

Query  1     tttttttCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTTTTTTCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCC   60

Query  61    ATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTCATTACaaaaatgaattataaaata   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTCATTACAAAAATGAATTATAAAATA   120

Query  121   taagttaaaagaaaaacataaaaCCCTACAATCTTACCCACCCAGACAACTACTATTAAT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TAAGTTAAAAGAAAAACATAAAACCCTACAATCTTACCCACCCAGACAACTACTATTAAT   180

Query  181   ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAA   240

Query  241   AATTATTCTTTACATATTGTTTTAAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AATTATTCTTTACATATTGTTTTAAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGC   300

Query  301   TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGA   360

Query  361   GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAG   420

Query  421   CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAAT   480
```

```
Query  481  CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCC  540

Query  541  TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA  575
            |||||||||||||||||||||||||||||||||||
Sbjct  541  TGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA  575
```

# Sequence 510 matched with Sequence 151

Query=   Sequence ID 510
Length=430


   SEQ ID NO: 151

ALIGNMENTS
 Identities = 430/430 (100%), Gaps = 0/430 (0%)

```
Query  1    CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTATGTTG  60

Query  61   TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAATANACGGG  120

Query  121  TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGGTCAGCTGGGCNC  180

Query  181  AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTGAGCAGATTGCTTGAGC  240

Query  241  CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCTATCNCTGTGAAAAATACAAA  300

Query  301  AAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTCCAGCTGCTTGAGAGTTTGAAGTGG  360

Query  361  GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGGATCACCTGAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGTGATCGCGTCACTGCACT  420

Query  421  CCAGCCTGGC    430
            ||||||||||
Sbjct  421  CCAGCCTGGC    430
```

# Sequence 512 matched with Sequence 152

```
Query=  Sequence ID 512
Length=631


   SEQ ID NO: 152

ALIGNMENTS
 Identities = 631/631 (100%), Gaps = 0/631 (0%)

Query  1    GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGGTCTT  60

Query  61   CAGGGTCTTCCATCTGGAACTATATAAAGTTCAGAAAACATGTCTCGAAGATATGACTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGGGTCTTCCATCTGGAACTATATAAAGTTCAGAAAACATGTCTCGAAGATATGACTCC  120

Query  121  AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATATGCCATGGAAGCT  180

Query  181  ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTTTTGCTTGCAGCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGGTGTTTTGCTTGCAGCA  240

Query  241  GAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCtttttttCTGAAAAAATTTATAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCTTTTTTTCTGAAAAAATTTATAAA  300

Query  301  CTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATAACTTCTGATGCTAATGTTCTGACT  360

Query  361  AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATGAACTAAGGCTCATTGCTCAAAGGTATTTATTACAGTATCAGGAGCCAATACCTTGT  420

Query  421  GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGCAGTTGGTTACAGCGCTGTGTGATATCAAACAAGCTTATACACAATTTGGAGGAAAA  480
```

```
Query  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CGTCCCTTTGGTGTTTCATTGCTGTACATTGGCTGGGATAAGCACTATGGCTTTCAGCTC  540

Query  541  TATCAGAGTGACCCTAGTGGAAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATCAGAGTGACCCTAGTGGAAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAAT  600

Query  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
            |||||||||||||||||||||||||||||||
Sbjct  601  ANCGCTGCAGCTGTGTCAATGTTGAAACAAG  631
```

# Sequence 513 matched with Sequence 153

Query=  Sequence ID 513
Length=646


   SEQ ID NO: 153

ALIGNMENTS
 Identities = 646/646 (100%), Gaps = 0/646 (0%)

```
Query  1     tttttttttATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCtttttttttCC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTTTTTTTTTATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCTTTTTTTTCC  60

Query  61    ACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTTGTCACATTCTT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTTGTCACATTCTT  120

Query  121   CATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAATTTGCATGCTTTA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAATTTGCATGCTTTA  180

Query  181   AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAATGCAGAGTCATGTATCC  240

Query  241   AAGATTACAATATCGCACAGAAGAGTTTCATCACTACTATATAAAACTCACCAGTCTTCCTCC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AAGATTACAATATCGCACAGAAGAGTTTCATCACTATATAAAACTCACCAGTCTTCCTCC  300

Query  301   TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAAACCACTCATATCTTT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAACTCCTTAAAACCACTCATATCTTT  360

Query  361   ACTATTGCTATAGTATTGCCTCTTCCACCATGTCATATAAATGGAAACATACAGTATTAG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ACTATTGCTATAGTATTGCCTCTTCCACCATGTCATATAAATGGAAACATACAGTATTAG  420

Query  421   TCTTCTCAAACTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCTTCTCAAACTAGTTTCTTTTACCTAACAACATGCATTTAAGATTCATAGTGTCTTTTA  480
```

```
Query  481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGACTTGATAGATTATTTCTTTGTAGCTGAATAATATTGCATCTTATAGATGTAACCGT  540

Query  541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGTATATCCATATTTTCTCACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCAT  600

Query  601  TCACAAAGCAGAAGTTTTAATTTTTATAAAGCTAATGNATCAACTT  646
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCACAAAGCAGAAGTTTTAATTTTTATAAAGCTAATGNATCAACTT  646
```

# Sequence 515 matched with Sequence 154

```
Query=   Sequence ID 515
Length=69


   SEQ ID NO: 154

ALIGNMENTS
 Identities = 69/69 (100%), Gaps = 0/69 (0%)

Query  1    CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACTGTTG  60

Query  61   AAACCTGCT  69
            |||||||||
Sbjct  61   AAACCTGCT  69
```

# Sequence 518 matched with Sequence 155

```
Query=   Sequence ID - 518                    nt:     502
Length=502


   SEQ ID NO: 155                 nt:     502

ALIGNMENTS
 Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query  1    GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTCAGAC  60

Query  61   TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGCTGCACGGT  120

Query  121  CTGAAACCACCTGTTCCCACCCTCTTGACCGAAATTTCCTTGTGACACAGAGAAGGGCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGAAACCACCTGTTCCCACCCTCTTGACCGAAATTTCCTTGTGACACAGAGAAGGGCAA  180

Query  181  AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTCAGGGTTCACTTCAGGGGCTCCCAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTCAGGGTTCACTTCAGGGGCTCCCAAA  240

Query  241  GCGACAAGATCGTTAGGGAGAGAGGCCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCGACAAGATCGTTAGGGAGAGAGGCCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGG  300

Query  301  GAACGGATCCCTTAGGTTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGGATCCCTTAGGTTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAA  360

Query  361  GGGTTGCTCTGCCCGCCGCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGTTGCTCTGCCCGCCGCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCC  420

Query  421  CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CAAAAGCCTGTGGCTTCAGTCCTGCGTCTGCACCACACATTCAAAAGGATCGTTTTGTTT  480
```

```
Query  481  TGTTTTTAAAGAAAGGTGANAT  502
            ||||||||||||||||||||||
Sbjct  481  TGTTTTTAAAGAAAGGTGANAT  502
```

Blast comparison trimmed "NAT" from the 3' end of both sequences and reported 499 identities. The report has been manually corrected for this. "NAT" has been appended to both sequences and identity count has been increased to 502.

# Sequence 519 matched with Sequence 156

```
Query=   Sequence ID 519
Length=373


   SEQ ID NO: 156

ALIGNMENTS
 Identities = 373/373 (100%), Gaps = 0/373 (0%)

Query  1    CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAGATCA  60

Query  61   TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTCATGANCAA  120

Query  121  ACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCATTTTGTCCAGCTGCCTGGAGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCATTTTGTCCAGCTGCCTGGAGCT  180

Query  181  GCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTTGTATGAATTTCTTTAT  240

Query  241  TTTAAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTAAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTAAGAGTTAACTGAAAGCTTNA  300

Query  301  GGAAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTACAAGTTACAATTCTATCACAGTTT  360

Query  361  TAAGATTATAAAC  373
            |||||||||||||
Sbjct  361  TAAGATTATAAAC  373
```

# Sequence 521 matched with Sequence 157

Query=   Sequence ID 521
Length=155


   SEQ ID NO: 157

ALIGNMENTS
 Identities = 155/155 (100%), Gaps = 0/155 (0%)

```
Query  1    GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTGTGAT  60

Query  61   ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTCCTGATGAG  120

Query  121  GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA  155
            |||||||||||||||||||||||||||||||||||
Sbjct  121  GGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA  155
```

## Sequence 523 matched with Sequence 158

```
Query=  Sequence ID - 523                    nt:      585
Length=585


   SEQ ID NO: 158                 nt:      585

ALIGNMENTS
 Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query  1    GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATATGCCA  60

Query  61   TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAATTCTGAGATTGAAGTCTTGAGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAATTCTGAGATTGAAGTCTTGAGAA  120

Query  121  CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAGGACCAGGGCTGC  180

Query  181  TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCAGGAGCTCTGGTGTCTG  240

Query  241  AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAAGTAAGAATCCGTCCTTCCTC  300

Query  301  CACTTTTTGTTCTATTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCCACACTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACTTTTTGTTCTATTCAGATGAGCCCTCAATGGACTGAACGATGCTCACCCACACTGT  360

Query  361  GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTCTTCTGGAAACACC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGGGCTGGTCTTCTTTATTCAATCCACTGACTTAAGTGCTGATCTCTTCTGGAAACACC  420

Query  421  TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTCACAGACACACCCAGAAATAATGTTCTACCAGCCATGGGCCTGTTACTTAGCCCAGTC  480
```

```
Query  481  AAGTTGACACAGAAAATTAGCTATCACAACATCtgtgtgtgtatatacatatgtatttgc  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAGTTGACACAGAAAATTAGCTATCACAACATCTGTGTGTGTATATACATATGTATTTGC  540

Query  541  atgtgtgtgtatatatggngtatatatattcatgtgtgtgtatat  585
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATGTGTGTGTATATATGGNGTATATATATTCATGTGTGTGTATAT  585
```

# Sequence 524 matched with Sequence 159

```
Query=   Sequence ID 524
Length=454


   SEQ ID NO: 159

ALIGNMENTS
 Identities = 454/454 (100%), Gaps = 0/454 (0%)

Query  1    CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCCTCTATCTTTTGGCATGACCCCAGAAGTCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCCTCTATCTTTTGGCATGACCCCAGAAGTCT  60

Query  61   TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTCCATATCCT  120

Query  121  GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTTGCTGATGATGCC  180

Query  181  ATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGATAATGCTTTTGTGTTC  240

Query  241  TCACATGTCCTGctctctctctctctctcATTTTGGTGTTGATCAGTCTTTCCATAAGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCACATGTCCTGCTCTCTCTCTCTCTCTCATTTTGGTGTTGATCAGTCTTTCCATAAGAT  300

Query  301  TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCTAAATTTACTCTTCTTGACTAGTAT  360

Query  361  CCTGTCACTTCTGAGGACTCATATTTTTGCAACTTGAAAATTATTCTTATTTATTTAAGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCTGTCACTTCTGAGGACTCATATTTTTGCAACTTGAAAATTATTCTTATTTATTTAAGT  420

Query  421  ATATGTTNCTGAAACTCTCATTAGACACATTTTG     454
            ||||||||||||||||||||||||||||||||||
Sbjct  421  ATATGTTNCTGAAACTCTCATTAGACACATTTTG     454
```

# Sequence 525 matched with Sequence 160

Query=   Sequence ID 525
Length=346


   SEQ ID NO: 160

ALIGNMENTS
 Identities = 346/346 (100%), Gaps = 0/346 (0%)

```
Query  1    GTTaaaaaaaGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTAAAAAAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCAC  60

Query  61   CTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTAACGGCCGC  120

Query  121  GGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAAATAGGGACCTGTATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAAATAGGGACCTGTATGA  180

Query  181  ATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGAAATTGACCTGCCCGTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGAAATTGACCTGCCCGTG  240

Query  241  AAGAGGCGGGCATAACACAGCTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGAGGCGGGCATAACACAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  300

Query  301  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaTTTT  346
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTT  346
```

## Sequence 526 matched with Sequence 161

```
Query=   Sequence ID - 526                    nt:     516
Length=516


   SEQ ID NO: 161                 nt:     516

ALIGNMENTS
 Identities = 516/516 (100%), Gaps = 0/516 (0%)

Query  1    CTTTTCATGGTCTCTTGTTCATTAATCATCTAAAATCCAAGCNCAGAGAATTCAATTTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTTCATGGTCTCTTGTTCATTAATCATCTAAAATCCAAGCNCAGAGAATTCAATTTTA  60

Query  61   GATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGATAATTAATA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGATAATTAATA  120

Query  121  TTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACACCCTATTTTCCTC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACACCCTATTTTCCTC  180

Query  181  CCCAGTGTTCTGACCGAGAGACTAATTAATAATTCAAGGAACTTACAGTGAATGANAACC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCAGTGTTCTGACCGAGAGACTAATTAATAATTCAAGGAACTTACAGTGAATGANAACC  240

Query  241  CATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAACAGCTGTCTCCCACATGGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAACAGCTGTCTCCCACATGGAT  300

Query  301  AGACACTTATTCCACCCATTTGCAGGTAGAATAGCTGGCAATAATAAGTCCTTCCCATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGACACTTATTCCACCCATTTGCAGGTAGAATAGCTGGCAATAATAAGTCCTTCCCATTG  360

Query  361  GATATGTTGAAAGGTGCCTGCCATGGCATAGTTGCCACAAGAGAGGAAGAAATGGACACA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATATGTTGAAAGGTGCCTGCCATGGCATAGTTGCCACAAGAGAGGAAGAAATGGACACA  420

Query  421  AATGTAGGCTGTTTTCAGGGCANAGGGAAGGTGGGAGGAAACCAANTTGCTGGTTTTCAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AATGTAGGCTGTTTTCAGGGCANAGGGAAGGTGGGAGGAAACCAANTTGCTGGTTTTCAC  480
```

```
Query  481  ACACCCTCTGGGGAACACCCATGCACCTATGANATG  516
            ||||||||||||||||||||||||||||||||||||
Sbjct  481  ACACCCTCTGGGGAACACCCATGCACCTATGANATG  516
```

# Sequence 527 matched with Sequence 162

```
Query=  Sequence ID 527
Length=385


   SEQ ID NO: 162

ALIGNMENTS
 Identities = 385/385 (100%), Gaps = 0/385 (0%)

Query  1    GACAAAAGCTGAGAGAAtttttttCTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAAAAGCTGAGAGAATTTTTTTCTTGAATATTTGCACTAAAAGATAGGTTAAAATTCT  60

Query  61   TCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAAGGAAGGAAGATTTG  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAAGGAAGGAAGATTTG  120

Query  121  GAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTTGGG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGGGACAGTTTTGGG  180

Query  181  AAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTGCTGCATCCACTGTGCA  240

Query  241  TCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGAAGTATAAACATGGACTAACA  300

Query  301  CAGAGATGGGCAAACTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGAGATGGGCAAACTACAGCCTGTGACCCAGCCACCTGTTTATGTAGAATCCAAAGTAA  360

Query  361  GAATCTTTAACTTACACATAAACTT  385
            |||||||||||||||||||||||||
Sbjct  361  GAATCTTTAACTTACACATAAACTT  385
```

# Sequence 530 matched with Sequence 165

```
Query=   Sequence ID - 530                    nt:      660
Length=660


   SEQ ID NO: 165                nt:     660

ALIGNMENTS
 Identities = 660/660 (100%), Gaps = 0/660 (0%)

Query  1    GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGAACCA  60

Query  61   TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGA  120

Query  121  TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAGAACTTAGATGTC  180

Query  181  AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATCAAAGAACTGAGAGTGA  240

Query  241  TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGTAAAGCTTTCTGATGGAAGAN  300

Query  301  AGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANAGGGTTGTGGANAAGTTTTTGAAGA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANAGGGTTGTGGANAAGTTTTTGAAGA  360

Query  361  GGGCTGAGAATTCATaaaaaaaaTTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGCTGAGAATTCATAAAAAAAATTCATTCTCTGTGGTATCCAAGAATCAGTGAAGATGCC  420

Query  421  AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTGAAACTTCAAGCAAATCTACTTCAACACTTCATGTATTGTGTGGGTCTGTTGTAGGG  480
```

```
Query  481  TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTTCAGTAAACAATGAATAGTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGCCAGATGCAATACAAGATTCCTGGTTAAATTTGAATTTCAGTAAACAATGAATAGTT  540

Query  541  TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTTCATTGTACCATGAAATATCCAGAACATACTTATATGTAAAGTATTATTTATTTGAAT  600

Query  601  CTACAAAAAACAACAAATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CTACAAAAAACAACAAATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA  660
```

## Sequence 532 matched with Sequence 166

Query=   Sequence ID 532
Length=542


   SEQ ID NO: 166

ALIGNMENTS
 Identities = 542/542 (100%), Gaps = 0/542 (0%)

```
Query  1    GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGGGAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGGGAGG  60

Query  61   GGAAACtttttttttttCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAAACTTTTTTTTTTTCTATAGACTTTTTTCANATAACATCTTCTGAGTCATAACCAGC  120

Query  121  CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAATTGATAAGTAAAG  180

Query  181  GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATAACCCTGAGATTCTTAC  240

Query  241  TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTAAGCAAATGAAAGCTACCAAT  300

Query  301  TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAAAGTTACGGAATCTACCATTTTAAAGTTAATTGCTTGTCAAGCTATAACCACAAAAA  360

Query  361  TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAAATACTGCTTTTAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAATGAATTGATGAGAAATACAATGAAGAGGCAATGTCCATCTCAAAATACTGCTTTTAC  420

Query  421  AAAAGCAGAATAAAAGCGAAAAGAAATGAAAATGTTACACTACATTAATCCTGGAATAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAAGCAGAATAAAAGCGAAAAGAAATGAAAATGTTACACTACATTAATCCTGGAATAAA  480
```

```
Query  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGCCGAAATAAATGAGAGATGAGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGT  540

Query  541  GT  542
            ||
Sbjct  541  GT  542
```

# Sequence 533 matched with Sequence 167

Query= Sequence ID 533
Length=421


SEQ ID NO: 167

ALIGNMENTS
Identities = 421/421 (100%), Gaps = 0/421 (0%)

```
Query  1    CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAGCCTC  60

Query  61   GGGGACAGAGCAAGACTCCATCTCAAAacacacacacacacacacacacacacacacaca  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGGACAGAGCAAGACTCCATCTCAAAACACACACACACACACACACACACACACACACA  120

Query  121  cacacaAAACAGATATACACTGAACACAGCACAAGTGGGACATAAGAGATTTAAAAGGGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACACAAAACAGATATACACTGAACACAGCACAAGTGGGACATAAGAGATTTAAAAGGGT  180

Query  181  TAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGATTTATCAACTGGATTC  240
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  181  TAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGATTTATCAACTGGATTC  240

Query  241  TGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACATAAAAAAGGGATACCATGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACATAAAAAAGGGATACCATGAG  300

Query  301  CAAAAGTATTTGAACATGGGCAATGGTTGAAACAAGTTTAAACAGATTATNTTTATTACC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAAAAGTATTTGAACATGGGCAATGGTTGAAACAAGTTTAAACAGATTATNTTTATTACC  360

Query  361  AAATCTCTCAAACCTTTAATATGCTATAAACATTGTGAAACAATaaaaaaaCTTTCCAAA  420
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  361  AAATCTCTCAAACCTTTAATATGCTATAAACATTGTGAAACAATAAAAAAAACTTTCCAAA  420

Query  421  A   421
            |
Sbjct  421  A   421
```

# Sequence 534 matched with Sequence 168

Query=   Sequence ID 534
Length=472


   SEQ ID NO: 168

ALIGNMENTS
 Identities = 472/472 (100%), Gaps = 0/472 (0%)

```
Query  1    GGGAAGGGAGCTATGAgtgtgtgtgttgtgtATGGACTCACTCCCAGGTTCACCTGGCCA  60
            |||||||||||||||| |||| | | || | |||||||||||||||||||||||||||||
Sbjct  1    GGGAAGGGAGCTATGAGTGTGTGTGTTGTGTATGGACTCACTCCCAGGTTCACCTGGCCA  60

Query  61   CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAAGTTTGCAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAAGTTTGCAG  120

Query  121  TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTTGCAGGCCTGCTT  180
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  121  TTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTTGCAGGCCTGCTT  180

Query  181  GCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTCAGGCACTGAGGGCCTG  240

Query  241  GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACTGAGTCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTACCCTATTTACAACTGAGTCA  300

Query  301  GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCAAGCCACTGATGGGAATATACAGATTTAGGTGCTAAACCGTTTATTTTCCACGGATG  360

Query  361  AGTCACAATCTGAAGAATCAAACTTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTCACAATCTGAAGAATCAAACTTCCATCCTGAAAATCTATATGTTTCAAAACCACTTG  420

Query  421  CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAGTA     472
            ||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  421  CCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGCCTCANACTGTGAAAGTA     472
```

## Sequence 560 matched with Sequence 169

Query= Sequence ID 560
Length=638


    SEQ ID NO: 169

ALIGNMENTS
 Identities = 638/638 (100%), Gaps = 0/638 (0%)

```
Query  1    GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAAGAGC  60

Query  61   AAAACTCCGTCTCaaaaaaaaaaaaaaaaaaaaaaaGCAATTTACTTAAAAACATACAAAC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAGCAATTTACTTAAAAACATACAAAC  120

Query  121  ACAGAGACAAGTATTTTTGAGAAACAAATACCtttttcattttttATACCAATGTAACAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACAGAGACAAGTATTTTTGAGAAACAAATACCTTTTTCATTTTTTATACCAATGTAACAA  180

Query  181  TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTGATATGATGAGGAAATA  240

Query  241  GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACTTTCACTGGGAAAAAAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACAACTTTCACTGGGAAAAAAGA  300

Query  301  TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTTGACAACAGTATGCTTATGTCTTAG  360

Query  361  AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTCATACCCACATTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTTTGAAATTCAAGTTCTTGAACATTATTAATGGCTACAATCATTCATACCCACATTGG  420

Query  421  GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCATTCTCCTCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCTGTATTCTTGATGAATCCAAAGTGATTTTCACCTCAACTCTGAATTTCATTCTCCTCT  480
```

```
Query  481  TTTGAATATAATACAACCATCTCACTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTGAATATAATACAACCATCTCACTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGAT  540

Query  541  TCATTATTGTTTTAGATAATGTTTTCATTTGCTTATGGGTATATAAAAAATTTTATCTTA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCATTATTGTTTTAGATAATGTTTTCATTTGCTTATGGGTATATAAAAAATTTTATCTTA  600

Query  601  AAAATATTTCCTCTCATTTAGCTAGCAACATTGTTTTC  638
            ||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAAATATTTCCTCTCATTTAGCTAGCAACATTGTTTTC  638
```

# Sequence 561 matched with Sequence 170

```
Query=   Sequence ID 561
Length=512


   SEQ ID NO: 170

ALIGNMENTS
 Identities = 512/512 (100%), Gaps = 0/512 (0%)

Query  1    CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCCACAT  60

Query  61   CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCAAGTCACAC  120

Query  121  CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCCCACCTTCTCCAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCCCACCTTCTCCAG  180

Query  181  AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGTTAAGGCACTTCTGCCA  240

Query  241  GCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGAGAGCCCCCTCTGTCACTGTG  300

Query  301  GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTGTTTCTCATCTGTGAAAGGTGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTTGTGTTTCTCATCTGTGAAAGGTGA  360

Query  361  TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAATGTGGGGCTGCTGTGAGATTTAAAGGACATAATGCACCTACGGTCCAAGCACTGCCT  420

Query  421  GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGAATACAGCANAAGCTCAACAGATACTGGACAACCCATCCCCTTAGTAGAGGCACTAAC  480
```

```
Query  481  CATGTGACCCAAGGCAAAAGTGCTTaaaaaaa  512
            ||||||||||||||||||||||||||||||||
Sbjct  481  CATGTGACCCAAGGCAAAAGTGCTTAAAAAAA  512
```

# Sequence 562 matched with Sequence 171

```
Query=   Sequence ID - 562                    nt:     580
Length=580


   SEQ ID NO: 171                    nt:     580

ALIGNMENTS
 Identities = 580/580 (100%), Gaps = 0/580 (0%)

Query  1    ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAAGCTG  60

Query  61   GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGGTTCCTGGC  120

Query  121  AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTTGCTGTTCGT  180

Query  181  GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGACAAGAAGGCTGCTGGA  240

Query  241  GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTA  300

Query  301  ATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGAACGGTCTCAGAACTGTTTGTTTCA  360

Query  361  ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTGGCCATTTAAGTTTAGTAGTAAAAGACTGGTTAATGATAACAATGCATCGTAAAACC  420

Query  421  TTCAGAAGGAAAGGAGAATgttttgtggaccactttggttttcttttttgcgtgtggcag  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTCAGAAGGAAAGGAGAATGTTTTGTGGACCACTTTGGTTTTCTTTTTTGCGTGTGGCAG  480
```

```
Query  481  ttttaagttattagtttttaaaatcagtactttttaATGGAAACAACTTGACCAAAAATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTTAAGTTATTAGTTTTTAAAATCAGTACTTTTTAATGGAAACAACTTGACCAAAAATT  540

Query  541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGTCACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAG  580
```

## Sequence 563 matched with Sequence 172

Query=  Sequence ID 563
Length=541


   SEQ ID NO: 172

ALIGNMENTS
 Identities = 541/541 (100%), Gaps = 0/541 (0%)

```
Query  1    GCAACCTGCACAACCCCGCCCTGTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCAACCTGCACAACCCCGCCCTGTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTGGCCG  60

Query  61   AGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGCCCACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCGGGCCCACC  120

Query  121  TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAGAGGAGCTGGCCA  180

Query  181  AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTGAAGCTGCGGTGTCAGG  240

Query  241  AGGAGATATCCAGGCAGGAGGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGAGATATCCAGGCAGGAGGGGAGCGAAGCCCACCGGCGACTTGCCCTTCCACTGGATCT  300

Query  301  GCCAGCCCTACATCCGGCCGGGGCCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCAGCCCTACATCCGGCCGGGGCCCAGGGAGGGGAGCAAGGAGAAGGCAGGTGCGCGCA  360

Query  361  GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGCACGGAGGTCCTGTCCAAGAACAAGCAAA  420

Query  421  AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAATATGCAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGAAGCAGCTGAGGAACCCCCACAAGACCTTCGACCCCTCTCTGAACCAAAATATGCAAA  480
```

```
Query  481  GTGTGACCAGTGTGGAAACCCAAAGGGCAACAGATGTGTGTTCAGCCTGTGCCGCGGNTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTGTGACCAGTGTGGAAACCCAAAGGGCAACAGATGTGTGTTCAGCCTGTGCCGCGGNTT  540

Query  541  G  541
            |
Sbjct  541  G  541
```

# Sequence 564 matched with Sequence 173

```
Query=   Sequence ID - 564                     nt:      671
Length=671


   SEQ ID NO: 173                  nt:     671

ALIGNMENTS
 Identities = 671/671 (100%), Gaps = 0/671 (0%)

Query  1     GGAATAGAATTTTAAATAGTAATAACTGCTTGttttttttGTGCAAGTACTTTTATACAT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGAATAGAATTTTAAATAGTAATAACTGCTTGTTTTTTTTGTGCAAGTACTTTTATACAT  60

Query  61    AAGATAAACAAAAACCTTACCACCAAACATACCAAAATGCACCTCTTTCATAAGTGAGTT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAGATAAACAAAAACCTTACCACCAAACATACCAAAATGCACCTCTTTCATAAGTGAGTT  120

Query  121   ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGATGTTTACATTTTA  180

Query  181   GGAAGGAAAATAGTTTTGTTTATTTAAACAACTGAATACTTATAAACTGTTGTTCCTGGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GGAAGGAAAATAGTTTTGTTTATTTAAACAACTGAATACTTATAAACTGTTGTTCCTGGA  240

Query  241   AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTCATGAATTTATAATTCCTAAATGAAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AGTTATTTATTCCATAAAAAATTTGTTCTTTTGTCATGAATTTATAATTCCTAAATGAAG  300

Query  301   ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGCTTTATTAATCAACTGATGTCTTGA  360

Query  361   TTTTTCTAAATGGGAAGATTGCTTTATTTTTAACACTAATTATGGGAGCAGATTCTTAGC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TTTTTCTAAATGGGAAGATTGCTTTATTTTTAACACTAATTATGGGAGCAGATTCTTAGC  420

Query  421   AAACTTCTTTGGAAAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAACTTCTTTGGAAAAGTTAATGTTATGATGTGCATTAGGCTGCCCCATCGTGTATATAA  480
```

```
Query  481  ATGAAGCAGATTTGATTTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGAAGCAGATTTGATTTTTGTATTCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACT  540

Query  541  TAAAGAAATACAGAATTTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAAAGAAATACAGAATTTCATATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGT  600

Query  601  AAATGGATTNAAAACTAACATGAAAAATATTCAACCTAAAAGAATTCTTAACTTCACAAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAATGGATTNAAAACTAACATGAAAAATATTCAACCTAAAAGAATTCTTAACTTCACAAG  660

Query  661  TGTTTTACTTC  671
            |||||||||||
Sbjct  661  TGTTTTACTTC  671
```

# Sequence 565 matched with Sequence 174

Query=  Sequence ID 565
Length=607


   SEQ ID NO: 174

ALIGNMENTS
 Identities = 607/607 (100%), Gaps = 0/607 (0%)

```
Query   1    CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTGCTAC   60

Query   61   AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCTGACAGTGA   120

Query   121  TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCACACAACAAGCCCA   180

Query   181  GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAACAGAGTCGGAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAGCAAAACAGAGTCGGAG   240

Query   241  TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTTCGGCAGGTTACAGGAGTTAC   300

Query   301  TAGAGTCACTATCCGGAAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TAGAGTCACTATCCGGAAATCTAAGAATATCCTCTTTGTCATCACAAAACCAGATGTCTA   360

Query   361  CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CAAGAGCCCTGCTTCAGATACTTACATAGTTTTTGGGGAAGCCAAGATCGAAGATTTATC   420

Query   421  CCAGCAAGCACAACTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAAA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CCAGCAAGCACAACTAGCAGCTGCTGAGAAATTCAAAGTTCAAGGTGAAGCTGTCTCAAA   480
```

```
Query  481  CATTCAAGAAAACACACAGACTCCAACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATTCAAGAAAACACACAGACTCCAACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGA  540

Query  541  TGAAACAGGTGTAGAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGAAACAGGTGTAGAAGTTAAGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTC  600

Query  601  GAGAGCA  607
            |||||||
Sbjct  601  GAGAGCA  607
```

# Sequence 566 matched with Sequence 175

Query=   Sequence ID 566
Length=583


   SEQ ID NO: 175

ALIGNMENTS
 Identities = 583/583 (100%), Gaps = 0/583 (0%)

```
Query  1    GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTCGCAGAGAtttttttttAAAGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTCGCAGAGATTTTTTTTAAAGGC  60

Query  61   ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAAATGTGTAT  120

Query  121  ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGATTAAAGGGAGAT  180

Query  181  CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAATAACAAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAAACAGTAAAATAACAAC  240

Query  241  AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCCATTATTGGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGATCTGAACACTGTCAACCATCTTGACAAATACTTATGCCTAGTGTTCCATTATTGGAA  300

Query  301  CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACTAAACATGTGGAATGATTTATATCCTACTGCTCAAGGTCATCACCAAGGTCTAATTG  360

Query  361  TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTTAATCGACATTTATAGCACAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAAAATTTCAAAAAATTGCAACCTCAGGCATAAATGGGTTAATCGACATTTATAGCACAC  420

Query  421  ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACATGCAACATGTACCAGAGATTCCTTCTTTTCTATGAACATGGTACTTCCACCAAGATA  480
```

```
Query  481  GACCACATTGTGAACTATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACCACATTGTGAACTATAAAACAAATCTAAAAACATTTGAAATGAAGGAAATTATATAA   540

Query  541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT   583
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AATATGTTCTCTTGATCTCAATGAAATTAAATTAATACTATAT   583
```

# Sequence 567 matched with Sequence 176

Query=  Sequence ID 567
Length=549


   SEQ ID NO: 176

ALIGNMENTS
 Identities = 549/549 (100%), Gaps = 0/549 (0%)

```
Query  1    CTCATGGCGGCCAATGTAGGCCCAAAACTTCCTCAAGTCAAACTCTCCAGGCCCACCTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCATGGCGGCCAATGTAGGCCCAAAACTTCCTCAAGTCAAACTCTCCAGGCCCACCTTC  60

Query  61   TGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGCAGGCCCTG  120

Query  121  CTCTTGCCTCCCAGGGGCTTTTTCCAGGCCCAGCTCTTGCCTCATGGCAGCTGCCCCAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCTTGCCTCCCAGGGGCTTTTTCCAGGCCCAGCTCTTGCCTCATGGCAGCTGCCCCAGG  180

Query  181  CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTCCTCCCTCACAGTGGCC  240

Query  241  CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGCCTAGTGCCTGCCTCGTGGCT  300

Query  301  GACTCTTGAAGCCCAAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GACTCTTGAAGCCCAAAACTTCCTCAAATCAGCCTTTTGCCCAACTTCTGTCTACTGTCG  360

Query  361  GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GACTCTACAGGTCAGCCTCTGCCTCACAGTGGACCCTCCAGACCCAGATGGTGTCTNCTG  420

Query  421  TGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGCATCCTCAGGCGAAGCTCCTGCCTTTCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGC  480
```

```
Query  481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCCAGCCTTCTCTCCAGGCTCTGAACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGA  540

Query  541  GTGTAGTAG  549
            |||||||||
Sbjct  541  GTGTAGTAG  549
```

# Sequence 568 matched with Sequence 177

Query= Sequence ID 568
Length=662


   SEQ ID NO: 177

ALIGNMENTS
 Identities = 662/662 (100%), Gaps = 0/662 (0%)

```
Query  1    TATATATGTAATGCCCTTAACCTAGTGTTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TATATATGTAATGCCCTTAACCTAGTGTTTGGCATGATCGTTGCTGAAAGGGAAGCTTGT  60

Query  61   GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGGTCAGGCTC  120

Query  121  CCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGACAGAGGCTCGGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGACAGAGGCTCGGGC  180

Query  181  TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCTAAGCCAGCAGGACAGC  240

Query  241  TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGGAACCATACA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGCACCTTTTTTGGAACCATACA  300

Query  301  GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTACTGGCAACCCCACTTGGTGGAGCA  360

Query  361  AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCAGCCATGGGGTCAGCCACACAGTCACCGC  420

Query  421  AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGCTGCTCTTTGGCACCGGGCGCTGGAAAGACCTAGGATGACACAGCCTGGAAAGAGCTT  480
```

```
Query  481  GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGAAAAGCTCATCTTCCACAGAACTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCC  540

Query  541  CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CACAACAGCCCTCTGTTGTAGGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGA  600

Query  601  ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ANACCCAGCTGAGGGCCTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTT  660

Query  661  AA  662
            ||
Sbjct  661  AA  662
```

# Sequence 570 matched with Sequence 178

```
Query=   Sequence ID 570
Length=339


   SEQ ID NO: 178

ALIGNMENTS
 Identities = 339/339 (100%), Gaps = 0/339 (0%)

Query  1    ACCGCGGCCGCGTnaanaaaaaaaaaaaaaGAATTCCACTTGATCAACTTAATTCCTTNT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCGCGGCCGCGTNAANAAAAAAAAAAAAAGAATTCCACTTGATCAACTTAATTCCTTNT  60

Query  61   CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTGTTTCGCTT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTGTTTCGCTT  120

Query  121  TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTTGTTTTCTCCTAA  180

Query  181  GTATTTGAGTTCAAAACTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAAGAAA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTATTTGAGTTCAAAACTCCTGTATCTAAAGAAATACGGTTGGGGTCATTAATAAAGAAA  240

Query  241  ATCTTTCTATCTTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATCTTTCTATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  300

Query  301  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  339
            |||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  339
```

# Sequence 571 matched with Sequence 179

```
Query=  Sequence ID - 571                    nt:     457
Length=457


   SEQ ID NO: 179                 nt:     457

ALIGNMENTS
 Identities = 457/457 (100%), Gaps = 0/457 (0%)

Query  1     TTAGAGAGGTGAGGATCTGGTATTTCCTGGACTAAATTCCCCTTGGGGAAGACGAAGGGA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTAGAGAGGTGAGGATCTGGTATTTCCTGGACTAAATTCCCCTTGGGGAAGACGAAGGGA  60

Query  61    TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCC  120

Query  121   CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCA  180

Query  181   GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAA  240

Query  241   ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGA  300

Query  301   GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCAATCATGTAAGTCTATATGACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAA  360

Query  361   ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTTCTATAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATTAAAAGTGATTGTTTCAAGGTGATGCAATTATTGATGACCTATTTTATTTTTCTATAA  420

Query  421   TGATCATATATTACCTTTGTAATAAAACATTTTTCCC    457
             |||||||||||||||||||||||||||||||||||||
Sbjct  421   TGATCATATATTACCTTTGTAATAAAACATTTTTCCC    457
```

# Sequence 572 matched with Sequence 180

```
Query=   Sequence ID 572
Length=658


   SEQ ID NO: 180

ALIGNMENTS
 Identities = 658/658 (100%), Gaps = 0/658 (0%)

Query  1     CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTAAGTT  60

Query  61    TGATTAGTGTTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGATTAGTGTTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTTATTGTTTA  120

Query  121   CTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATGAGATCTCTNNTT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATGAGATCTCTNNTT  180

Query  181   GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGACCAGATGACTTATAGG  240

Query  241   TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTTTGAGGTACTTAATCTATATA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTTTGAGGTACTTAATCTATATA  300

Query  301   AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCTCATGTCTAAAGTCTGATTGATTAA  360

Query  361   ATTCATTCTTGGTATTTCATTTTGAAAAGAATGTAGCTTTAGCAAACCTCTTTGTATAAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATTCATTCTTGGTATTTCATTTTGAAAAGAATGTAGCTTTAGCAAACCTCTTTGTATAAA  420

Query  421   TGCAGTGGGATTAAGGTCatttaaaaaattgttatatcattgtatttttaaaatttacca  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TGCAGTGGGATTAAGGTCATTTAAAAAATTGTTATATCATTGTATTTTTAAAATTTACCA  480
```

Page 298

```
Query  481   gttttatttttcttttacccttaGCCCGGCCTCAGAAAGTGTGTTTGTGTCCATTTCT   540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GTTTTATTTTTCTTTTTACCCTTTAGCCCGGCCTCAGAAAGTGTGTTTGTGTCCATTTCT   540

Query  541   CCCAGCGCACCCTCTGCATATCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAA   600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CCCAGCGCACCCTCTGCATATCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAA   600

Query  601   AACAAAGTGTTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA   658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   AACAAAGTGTTGCGTACAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA   658
```

# Sequence 574 matched with Sequence 181

```
Query=   Sequence ID 574
Length=452


   SEQ ID NO: 181

ALIGNMENTS
 Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query  1    TTATTGCTGACATAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTATTGCTGACATAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAATCTG  60

Query  61   CACCATTTATACATGGAACTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CACCATTTATACATGGAACTGGAGAACATTGTGCCAATAATCATTTAATATATGCCAAAT  120

Query  121  CTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGAGGGCTAAAGATT  180

Query  181  GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTCANAGCAGAGTTCTTGTTGTGGGTAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTCANAGCAGAGTTCTTGTTGTGGGTAG  240

Query  241  ACTGTGACTAGGTTCACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTGTGACTAGGTTCACAGCCTTTGTGGAACATTCCGTATAACGGCATTGTGGAAGCAAT  300

Query  301  AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGATGGCTGGGAAGCCAGGCCAAAGTGG  360

Query  361  GGGCAACAGCTTGCTTCTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGCAACAGCTTGCTTCTCTCTTTCTCTTCTCACCCTCAGTTTGTATGGGAAAATGGAGATG  420

Query  421  TCCTCTCCACTTTATCCCACGATATCTAAATG    452
            ||||||||||||||||||||||||||||||||
Sbjct  421  TCCTCTCCACTTTATCCCACGATATCTAAATG    452
```

# Sequence 575 matched with Sequence 182

```
Query=  Sequence ID - 575                  nt:     209
Length=188


  SEQ ID NO: 182                 nt:     209

ALIGNMENTS
 Identities = 188/188 (100%), Gaps = 0/188 (0%)

Query  1    CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATACAAAA  60

Query  61   AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCTTAGGCAGG  120

Query  121  AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGCACCATTGCACTC  180

Query  181  CACCCTGG  188
            ||||||||
Sbjct  181  CACCCTGG  188
```

## Sequence 576 matched with Sequence 183

```
Query=   Sequence ID - 576                      nt:     541
Length=541


   SEQ ID NO: 183                   nt:     541

ALIGNMENTS
 Identities = 541/541 (100%), Gaps = 0/541 (0%)

Query  1    CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGCCACG  60

Query  61   AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCCTGTTGCGG  120

Query  121  GTAAAAATAACCAAATTATCAGTCCTTGGAAACCCAGGCAATCAAGTGAGTACAAGGTAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTAAAAATAACCAAATTATCAGTCCTTGGAAACCCAGGCAATCAAGTGAGTACAAGGTAA  180

Query  181  AGATAAGTATGGTTTAGAGGAGAAATTATGTTCCTGAACTGGTGTCCTTTGATGGCAGCG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGATAAGTATGGTTTAGAGGAGAAATTATGTTCCTGAACTGGTGTCCTTTGATGGCAGCG  240

Query  241  TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTAATAAGCTTTGGTGAGCATCA  300

Query  301  TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGCTTTTAAAAGTGCTTTTGCAGACCC  360

Query  361  TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGGAAGGGATCCTCCACACATATGAGGTGTGGGACAGGTAGGCCAGAGAGGATTAGCCCT  420

Query  421  GCTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCTTTCGAGACTAGAAATCTACAGTCCTGAAGGAGCAGTAATTAATTGGTACACCTGTCA  480
```

```
Query   481   GGGCCAGCCCCCAGGTCTCCTGGCTTTTTCCAGGTTTTCTGTCTCACATGATTTTGCTTT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GGGCCAGCCCCCAGGTCTCCTGGCTTTTTCCAGGTTTTCTGTCTCACATGATTTTGCTTT   540

Query   541   T   541
              |
Sbjct   541   T   541
```

# Sequence 577 matched with Sequence 184

Query=  Sequence ID 577
Length=640


   SEQ ID NO: 184

ALIGNMENTS
 Identities = 640/640 (100%), Gaps = 0/640 (0%)

```
Query  1    CTTTAATTTTTCAAGTGTTTAAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTAATTTTTCAAGTGTTTAAAAAACAATTTTATACTTAAGCCAGCCTTGAAGATAAGC  60

Query  61   ACAAAATTTACCAGTTTACATTTaaaaaacaaacaaaaaaCGACAACAACTCAAGCACCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAAAATTTACCAGTTTACATTTAAAAAACAAACAAAAAACGACAACAACTCAAGCACCC  120

Query  121  GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACCTTAGAAATATGA  180

Query  181  GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAATAAAATCACC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAAAATAAATAAAATCACC  240

Query  241  ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCACAGAAAGGCTAATTTCTGCC  300

Query  301  AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCCAAAAACACGAAAGCAGAATTCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCCCAAAAACACGAAAGCAGAATTCCT  360

Query  361  TTTCACTGaaaaaaaTAAACAGTTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTAttt  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTCACTGAAAAAAATAAACAGTTTTCCATGCAAGGGCAGTTTGCTTCTAATAAGTATTT  420

Query  421  tttaaaaaatttttttttCCTCTAGCTTTTCTTTAAATTTTCTTCCTCTAATATTGCCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTAAAAAATTTTTTTTTCCTCTAGCTTTTCTTTAAATTTTCTTCCTCTAATATTGCCTT  480
```

```
Query  481  TTCTTGTACAAGGCAGACCAGGTATCTTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCTTGTACAAGGCAGACCAGGTATCTTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTA  540

Query  541  TTGCATCTTGAAGACAAACCATTTCCCAGAGTAGTGATAAAAAATAACACTaaaaaaaCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGCATCTTGAAGACAAACCATTTCCCAGAGTAGTGATAAAAAATAACACTAAAAAAACT  600

Query  601  TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA  640
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTAAAGGTGAGTCACTTCATCACCTTGATGAAGTAAAAAA  640
```

# Sequence 578 matched with Sequence 185

Query=  Sequence ID 578
Length=633


   SEQ ID NO: 185

ALIGNMENTS
 Identities = 633/633 (100%), Gaps = 0/633 (0%)

```
Query  1    GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTACTTGT  60

Query  61   TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGTATCATGGT  120

Query  121  TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAACCCAAAGAAAAT  180

Query  181  TCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAGCAAAAGAAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTATATAAAAGCAAAAGAAC  240

Query  241  TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTTGAATATATTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAGTTACTGATTTGAATATATTA  300

Query  301  TATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAGTACATTAGAGAACCTGTGTTTCCT  360

Query  361  CTCTCCTCTACCATTCATCTCTCTTCCATACAGTCATTTGGGCTTTTTACTCAAAGAGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCTCCTCTACCATTCATCTCTCTTCCATACAGTCATTTGGGCTTTTTACTCAAAGAGAA  420

Query  421  TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTaaaaaaaaattttt  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TCAAGAAATAATAAGGTATAACAAGCTTGGCAAAGTGTTGGCTTTTTAAAAAAAAATTTT  480
```

```
Query  481  tttAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTAATCTCTAGCAGTTTGGTAATTTAGCAGCATCATTTATTTGGGATTCTTTTATCTGA  540

Query  541  TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTCCAAAAGATGGAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTTCAACAGTGAAAAACATCCCTATGATAAAGCCTAATGACCCATTTCCAAAAGATGGAA  600

Query  601  TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT  633
            |||||||||||||||||||||||||||||||||
Sbjct  601  TTGCCCTTCCTAGAAAATATGACGGAGAAAAGT  633
```

# Sequence 579 matched with Sequence 186

```
Query=  Sequence ID - 579                    nt:     502
Length=502


   SEQ ID NO: 186                  nt:     502

ALIGNMENTS
 Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query  1    CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACAGTCT  60

Query  61   TGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTTATGTTGTC  120

Query  121  AAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAACTAGAATGAAAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAACTAGAATGAAAA  180

Query  181  CAAAAACGTTCCTTGTATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAAAAACGTTCCTTGTATAATATTCATTANAAAGAAATGAAGAAGGCCGGGCATGGTGGC  240

Query  241  TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGGCAGATCATGAGGTCAGGAGT  300

Query  301  TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAATACAaaaaaaTTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTCTCTACCAAAAATACAAAAAAATTA  360

Query  361  GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCGGGCATGGTGGCACACACCTGTCATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAT  420

Query  421  TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGCTTGAACCTGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGTACTACAGCC  480
```

```
Query  481  TAGGTGACAGTGCAAGACTCTG  502
            ||||||||||||||||||||||
Sbjct  481  TAGGTGACAGTGCAAGACTCTG  502
```

# Sequence 580 matched with Sequence 187

```
Query=  Sequence ID - 580               nt:     316
Length=316


   SEQ ID NO: 187                nt:     316

ALIGNMENTS
 Identities = 316/316 (100%), Gaps = 0/316 (0%)

Query  1    CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNGGATT  60

Query  61   aaaaaaaCACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAAAACACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATCACCTACAA  120

Query  121  TTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACCACTTATCTTGAG  180

Query  181  CTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGAAATATCAAATCAATGG  240

Query  241  TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCAACTTTGTAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACTTGGTTTAAGCAACTTTGTAT  300

Query  301  AATTNACCTCCTAAAT  316
            ||||||||||||||||
Sbjct  301  AATTNACCTCCTAAAT  316
```

# Sequence 581 matched with Sequence 188

Query=   Sequence ID 581
Length=94


   SEQ ID NO: 188

ALIGNMENTS
 Identities = 94/94 (100%), Gaps = 0/94 (0%)

Query  1    CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACA  60

Query  61   TCCAGTCAGTCACTCATCAACTCTATTGATTCTG  94
            ||||||||||||||||||||||||||||||||||
Sbjct  61   TCCAGTCAGTCACTCATCAACTCTATTGATTCTG  94

## Sequence 582 matched with Sequence 189

Query= Sequence ID 582
Length=644


   SEQ ID NO: 189

ALIGNMENTS
 Identities = 644/644 (100%), Gaps = 0/644 (0%)

```
Query  1    TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTCCTTCTCTGTCTTCTGTGGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTCCTTCTCTGTCTTCTGTGGGC  60

Query  61   TTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCCTCTCATGGGCTTCCTTCCCTTCTCAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCCTCTCATGGGCTTCCTTCCCTTCTCAG  120

Query  121  CTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCCTCTCTATCTCTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCCTCTCTATCTCTA  180

Query  181  TGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGGAATTTCCATTTGTGCATCCCAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGGAATTTCCATTTGTGCATCCCAT  240

Query  241  GCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTCAGCCCTACCCCAGTCCTCAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTCAGCCCTACCCCAGTCCTCAGA  300

Query  301  AAAGTTCCTCTCCCTGGATCCTCTTTTTCCTTCATGAGTGCCCGGTTGCCCAAGTCAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAGTTCCTCTCCCTGGATCCTCTTTTTCCTTCATGAGTGCCCGGTTGCCCAAGTCAAAA  360

Query  361  ACCTGGGAGTGATATAAACTCCCCACACATCCAGTCAGTCACTCATCAACTCTATTGATT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACCTGGGAGTGATATAAACTCCCCACACATCCAGTCAGTCACTCATCAACTCTATTGATT  420

Query  421  CTGTCTGCTAAATATATCTCAATTGTATTAACTTAAACATATGCATAATACATCTTCTTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTGTCTGCTAAATATATCTCAATTGTATTAACTTAAACATATGCATAATACATCTTCTTC  480
```

```
Query  481  TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCACTGCATTTTTGTGGGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTT  540

Query  541  GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCCCTTCTAGTCAGAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAAC  600

Query  601  ATTACACTGAATGTGCAAAACTGGAAGGGCATCCAAACAGAGGA  644
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ATTACACTGAATGTGCAAAACTGGAAGGGCATCCAAACAGAGGA  644
```

## Sequence 583 matched with Sequence 190

```
Query=   Sequence ID - 583                    nt:      631
Length=631


   SEQ ID NO: 190                  nt:     631

ALIGNMENTS
 Identities = 631/631 (100%), Gaps = 0/631 (0%)

Query  1    CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCATTTTCAGTTTCTCCAGTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCATTTTCAGTTTCTCCAGTTA  60

Query  61   GTAACTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTTAAGTGAGAAATCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAACTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTTAAGTGAGAAATCT  120

Query  121  ATAAAAAGAACCATGTTAACATAAATATTTCAGTCCTTACAAGTTGGTATTGACTTTTCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATAAAAAGAACCATGTTAACATAAATATTTCAGTCCTTACAAGTTGGTATTGACTTTTCT  180

Query  181  CATTGGTAATCTGACTGATTTAATACTGCTCATTCCAATATCTGGTGATGTAATTCTGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATTGGTAATCTGACTGATTTAATACTGCTCATTCCAATATCTGGTGATGTAATTCTGGT  240

Query  241  TATGAATCCTTGTATTAATAACACCTCCTGGGAGGtttttttttCCCCAACATTACATTCA  300
            |||||||||||||||||||||||||||||||||| | |||||||||||||||||||||||
Sbjct  241  TATGAATCCTTGTATTAATAACACCTCCTGGGAGGTTTTTTTTTCCCCAACATTACATTCA  300

Query  301  GAATATTAGAGCTGAAAATACCTTTTTTAAGGTTATCAGGAGGAGGGAGCTTATGTTTAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAATATTAGAGCTGAAAATACCTTTTTTAAGGTTATCAGGAGGAGGGAGCTTATGTTTAA  360

Query  361  TGTGGTGGATAAAACTTAACTGCTGGTTAATACAATTGTTATTCAGGTGAAATTCCCTAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGTGGTGGATAAAACTTAACTGCTGGTTAATACAATTGTTATTCAGGTGAAATTCCCTAA  420

Query  421  ACTTTTCACGTGCAAAGTTTTGTATGTATACAGACATTTGGGGAAAAGTTTTATCATCCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACTTTTCACGTGCAAAGTTTTGTATGTATACAGACATTTGGGGAAAAGTTTTATCATCCC  480
```

```
Query  481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAAACCGGTTACTGTCCAGAAAATGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGG  540

Query  541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATTTATTCATTTATTTATTCAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACA  600

Query  601  CTGACATTCTGCTTCTAATCTAACCGAAAT  631
            ||||||||||||||||||||||||||||||
Sbjct  601  CTGACATTCTGCTTCTAATCTAACCGAAAT  631
```

# Sequence 585 matched with Sequence 191

```
Query=  Sequence ID 585
Length=638


   SEQ ID NO: 191

ALIGNMENTS
 Identities = 638/638 (100%), Gaps = 0/638 (0%)

Query  1    TTTCAAATTGTACAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGATTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTCAAATTGTACAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGATTAA  60

Query  61   TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAA  120

Query  121  ATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC  180

Query  181  TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTATGCA  240

Query  241  AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTATTTGTGAA  300

Query  301  AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAAAAGCTTACTTTA  360

Query  361  GCACTCATCTTTTACATGGTTAAATGCATTTCCTAATTTGAGATCACCTAAACACTGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCACTCATCTTTTACATGGTTAAATGCATTTCCTAATTTGAGATCACCTAAACACTGGAA  420

Query  421  AAGaaaaaaaaTGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGAAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACAAATAATTTGGCTGTAATGTA  480
```

```
Query  481  TCATaaaacacaaaccccacacatctgtacaataaacattatgtattacatacacacaac  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCATAAAACACAAACCCCACACATCTGTACAATAAACATTATGTATTACATACACACAAC  540

Query  541  acacacCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACACACCCAGTCATAAAGCCTAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCAT  600

Query  601  TTTTTCTTATTTCATCAAATGAATAGCTTTTTGTCACC  638
            ||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTTTTCTTATTTCATCAAATGAATAGCTTTTTGTCACC  638
```

# Sequence 586 matched with Sequence 192

```
Query=  Sequence ID 586
Length=283


   SEQ ID NO: 192

ALIGNMENTS
 Identities = 283/283 (100%), Gaps = 0/283 (0%)

Query  1    GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGTGGTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGTGGTA  60

Query  61   TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAACTGTTCAC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAACTGTTCAC  120

Query  121  TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAAGAAGTAGTTCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAAGAAGTAGTTCCA  180

Query  181  AACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAGAGAGCAGCTTTAAAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAGAGAGCAGCTTTAAAAG  240

Query  241  GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT     283
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGAGAT     283
```

# Sequence 587 matched with Sequence 193

Query=  Sequence ID 587
Length=613


   SEQ ID NO: 193

ALIGNMENTS
 Identities = 613/613 (100%), Gaps = 0/613 (0%)

```
Query  1    tttttttttttCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGCTGAC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTTTCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGCTGAC  60

Query  61   TCCAAGGNACACACAGTCCTGTATCTGGAACTACTGAGTGGCAGGCATCTTTCTCTGCCT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCAAGGNACACACAGTCCTGTATCTGGAACTACTGAGTGGCAGGCATCTTTCTCTGCCT  120

Query  121  CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAAGGTCTCAGCGGG  180

Query  181  TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTTAATATTTTATAATCTTGACA  240

Query  241  TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGTATTCACTTACCTT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGACACCAAGATGCTTTAATAAAAAAGCACCTCTAACTCGGTCTTGTATTCACTTACCTT  300

Query  301  GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAACA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAACAGGTAGAGGGGAGATGGTGGAACA  360

Query  361  TAAAACACAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCCATGACCAGGTCTTTCAA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAAAACACAATTTTGCTTGGCACCCACCTTGGCGTCTGTCCCCATGACCAGGTCTTTCAA  420

Query  421  TTCGATGATTTTGTCATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTCGATGATTTTGTCATTGATGGAGGAGCGATATCGTTTCTCAATGATATTATGGGTTGT  480
```

```
Query  481  CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCGCCTTTCTCCTTCTTTGGGGGGCTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAAT  540

Query  541  GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGGGCACTTTCTCTTGCCCCATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGC  600

Query  601  CCACCAGGGTCTA  613
            |||||||||||||
Sbjct  601  CCACCAGGGTCTA  613
```

# Sequence 588 matched with Sequence 194

```
Query=   Sequence ID 588
Length=350


   SEQ ID NO: 194

ALIGNMENTS
 Identities = 350/350 (100%), Gaps = 0/350 (0%)

Query  1    CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGTCCAT  60

Query  61   ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGGCTGAGGCA  120

Query  121  GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCGTCTCT  180

Query  181  ACTaaaaaaaatattaaaaaaTTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACTAAAAAAAATATTAAAAAATTGGCCAGGCCTGGTGGTGGGCGCCTGTGGTCCCGGCTG  240

Query  241  CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAGTCGGAGGTTGCAGTGAGCCA  300

Query  301  AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCaaaaaaaaaaaaaa  350
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGATTGCACCTGGGCAACACAGCGAGACTCCGTCTCAAAAAAAAAAAAAA  350
```

# Sequence 589 matched with Sequence 195

Query=   Sequence ID 589
Length=541


   SEQ ID NO: 195

ALIGNMENTS
 Identities = 541/541 (100%), Gaps = 0/541 (0%)

```
Query  1    CAATTATTTATTACCTTTCCATTTGTTCGCCTGATGATGTGACAATGCATGGTCTTTGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAATTATTTATTACCTTTCCATTTGTTCGCCTGATGATGTGACAATGCATGGTCTTTGTG  60

Query  61   CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTTACATTCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTTTACATTCA  120

Query  121  TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAACCTCTTATAAAT  180

Query  181  GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAGAAAAAATGCTTTTCTT  240

Query  241  TGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGTGGAAACCCTAGGCTCTGAGA  300

Query  301  CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACACTCTCTGGTGTCTGAGACAGAACCAAAGCAATAACGTTGTGATGCCCACAGGCCTG  360

Query  361  GAGCCAGCTAGCGACCTTGTGCCGCCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGCCAGCTAGCGACCTTGTGCCGCCCAGCTGTCCATGGCCCGTGCAGAGCAGAGGACAG  420

Query  421  TGAGTGTCTGCACTGAGAACCTTAAACCACAGTTGAACATACCCACACCTGTTTGTCTTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAGTGTCTGCACTGAGAACCTTAAACCACAGTTGAACATACCCACACCTGTTTGTCTTA  480
```

```
Query  481  AGCTATAGTGTAAAAACAAAGTTTGGGCTCTGAAAATTTAACTGAAAAAGATTTCCTTGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCTATAGTGTAAAAACAAAGTTTGGGCTCTGAAAATTTAACTGAAAAAGATTTCCTTGT  540

Query  541  T  541
            |
Sbjct  541  T  541
```

# Sequence 590 matched with Sequence 196

```
Query=  Sequence ID 590
Length=336


   SEQ ID NO: 196

ALIGNMENTS
 Identities = 336/336 (100%), Gaps = 0/336 (0%)

Query  1    GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCT  60

Query  61   GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC  120

Query  121  CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAA  180

Query  181  AACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCG  240

Query  241  ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGT  300

Query  301  GGAATATTTGTCATAAATAAATAATGAAAACCTAAA    336
            ||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAATATTTGTCATAAATAAATAATGAAAACCTAAA    336
```

# Sequence 591 matched with Sequence 197

```
Query=   Sequence ID 591
Length=377


   SEQ ID NO: 197

ALIGNMENTS
 Identities = 377/377 (100%), Gaps = 0/377 (0%)

Query  1    CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCCATCA   60

Query  61   GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGTAGGGAGGT   120

Query  121  TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGATCACTGTGCAGTG   180

Query  181  GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCAGTGGTCAAAATAC   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTTTCAGTGGTCAAAATAC   240

Query  241  TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCATGGAGGTGCTGAACACAGGG   300

Query  301  AAGGTCTGGTACATATTGGAAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGGTCTGGTACATATTGGAAATTATGAGCAGAACAAATACTCAACTAAATGCACAAAGT   360

Query  361  ATAAAGTGTAGCCATGT   377
            |||||||||||||||||
Sbjct  361  ATAAAGTGTAGCCATGT   377
```

# Sequence 592 matched with Sequence 198

Query=   Sequence ID 592
Length=63


   SEQ ID NO: 198

ALIGNMENTS
 Identities = 63/63 (100%), Gaps = 0/63 (0%)

```
Query  1    TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGaaaaaaaaaaa  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAAAAAAA  60

Query  61   aaa  63
            |||
Sbjct  61   AAA  63
```

# Sequence 593 matched with Sequence 199

Query=  Sequence ID – 593                        nt:     565
Length=565


   SEQ ID NO: 199                    nt:     565

ALIGNMENTS
 Identities = 565/565 (100%), Gaps = 0/565 (0%)

Query  1    CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCAAACTCTGTCTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCAAACTCTGTCTC  60

Query  61   AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGTTGGAGCAG  120

Query  121  CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGATCCTTTGGCATC  180

Query  181  CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGCCAAGGCAGAAGAAATC  240

Query  241  TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAAACAACTTCTCAGATACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAAAAAACAACTTCTCAGATACT  300

Query  301  GGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAAACTTTGGTTTTGGGATCCAGGAACACATCGATCTGGGTATCAAATATGACCCAAGC  360

Query  361  ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTGGTATCTACGGCCTGGACTTCTATGTGGTGCTGGGTAGGCCAGGTTTCAGCATCGCA  420

Query  421  GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GACAAGAAGCGCAGGACAGGCTGCATTGGGGCCAAACACAGAATCAGCAAAGAGGAGGCC  480

```
Query  481  ATGCGCTGGTTCCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGCGCTGGTTCCAGCAGAAGTATGATGGGATCATCCTTCCTGGCAAATAAATTCCCGTT   540

Query  541  TCTATCCAAAAGAGCAATAAAAAGT   565
            |||||||||||||||||||||||||
Sbjct  541  TCTATCCAAAAGAGCAATAAAAAGT   565
```

# Sequence 594 matched with Sequence 200

```
Query=  Sequence ID 594
Length=629


   SEQ ID NO: 200

ALIGNMENTS
 Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query  1    CAGAAGAGTAAGCAAATCTCaaagcagcgaaagggaagaaactaaaaaaggtagagcaga  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAAGAGTAAGCAAATCTCAAAGCAGCGAAAGGGAAGAAACTAAAAAAGGTAGAGCAGA  60

Query  61   aataagagaaaatagagaagagaacaattgagaaaaataattgaaaccaaaaGGTGGTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATAAGAGAAAATAGAGAAGAGAACAATTGAGAAAAATAATTGAAACCAAAAGGTGGTTC  120

Query  121  TTTGAAAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAAGGGCAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTGAAAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAGAAAAAAGGGCAG  180

Query  181  TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACTACCAATTTACAGAAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACTACCAATTTACAGAAAT  240

Query  241  AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAACTTAGAAGAATATATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAAAGGATTATGAGGAAATACTACAGATAATTGATGACATTAACTTAGAAGAATATATT  300

Query  301  TCAAGAAAGACACAAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCAAGAAAGACACAAACTACTGAAACCGACTCAAGAAGAAACAGAAAATCTGAACAGACC  360

Query  361  TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TATAAAAAATAGAGATTTAATTGATATTCAGAAAGTTTCCCAAAAAGAAAAGCACTGGCC  420

Query  421  AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGATGACTTCACTGGTGAATTCTATCAAGTGTCAAAGATGAATTACTGACATTCATTCA  480
```

```
Query   481   CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT   540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   CACTCCTTTAAGAAATAGAAGAGGGGACATCACTTTTCAAAGCATCGACATTCTAATCAT   540

Query   541   TAGTCCCTTGGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACaaaaaaaCCCCTACAGA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   TAGTCCCTTGGTTTCCTGCTCCCAAAGCCAGGTGATGTATCACAAAAAAAACCCCTACAGA   600

Query   601   CCCACTGGGCACAATGGCTTTATGCCTAT   629
              |||||||||||||||||||||||||||||
Sbjct   601   CCCACTGGGCACAATGGCTTTATGCCTAT   629
```

# Sequence 595 matched with Sequence 201

```
Query=  Sequence ID - 595                nt:    98
Length=98


   SEQ ID NO: 201              nt:    98

ALIGNMENTS
 Identities = 98/98 (100%), Gaps = 0/98 (0%)

Query  1    CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTTCCATCCATGCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTTCCATCCATGCTG  60

Query  61   ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA  98
            ||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA  98
```

# Sequence 596 matched with Sequence 202

Query= Sequence ID 596
Length=224


   SEQ ID NO: 202

ALIGNMENTS
 Identities = 224/224 (100%), Gaps = 0/224 (0%)

```
Query  1    CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGGTAGG  60

Query  61   GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACTCTGGGAAATGGTAAGACAGGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACTCTGGGAAATGGTAAGACAGGG  120

Query  121  AAAGGCCATGTTGTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAGGCCATGTTGTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAGAGAGAACAGTTA  180

Query  181  GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT    224
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT    224
```

# Sequence 597 matched with Sequence 203

```
Query=   Sequence ID 597
Length=81


   SEQ ID NO: 203

ALIGNMENTS
 Identities = 81/81 (100%), Gaps = 0/81 (0%)

Query  1    CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATaaaaa   60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATAAAAA   60

Query  61   aaaaaaaaanaaaaaaaaaaa   81
            |||||||||||||||||||||
Sbjct  61   AAAAAAAAANAAAAAAAAAAA   81
```

# Sequence 598 matched with Sequence 204

```
Query=   Sequence ID - 598                 nt:      362
Length=362


   SEQ ID NO: 204                 nt:      362

ALIGNMENTS
 Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query  1    GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGTTCAA  60

Query  61   GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACTAAAACGCT  120

Query  121  GTCTCaaaaaaaaaacaaaaacgacnaaaaaaaaacaaaacagaaaaaaTTAACTTAGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTCTCAAAAAAAAAACAAAAACGACNAAAAAAAAACAAAACAGAAAAAATTAACTTAGGC  180

Query  181  AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTCAAGGAAGGTAACCCTG  240

Query  241  AANCAGGACTTGTAAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AANCAGGACTTGTAAAGCAAATAANATTGGGAGGCCAAGGTGGGTGGATCACNAGGTCAG  300

Query  301  GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACaaaaaaa  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGTTCGAGACCAACCTGGCCAACATAGTGAAACCCCGTCTTTCTAAAAATACAAAAAAA  360

Query  361  TT   362
            ||
Sbjct  361  TT   362
```

## Sequence 599 matched with Sequence 205

Query=   Sequence ID 599
Length=581


   SEQ ID NO: 205


ALIGNMENTS
 Identities = 581/581 (100%), Gaps = 0/581 (0%)

```
Query   1    GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCTTCCT   60

Query   61   AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGACACACGAGC   120

Query   121  ATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAAGTATTTAGCTG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAAGTATTTAGCTG   180

Query   181  ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTCTGAGCCCTAGG   240

Query   241  ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACTCATCACT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  ATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCAAACTCATCACT   300

Query   301  AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AGACATCGTACTACACGACACGTACTACGTTGTAGCTCACTTCCACTATGTCCTATCAAT   360

Query   361  AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGGCTA   420

Query   421  CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCT   480
```

```
Query  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACTTTCTTCCCACAACACTTTCTCGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTA  540

Query  541  CCCCGATGCATACACCACATGAAACATCCTATCATCTGGAG  581
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCCCGATGCATACACCACATGAAACATCCTATCATCTGGAG  581
```

# Sequence 600 matched with Sequence 206

```
Query=  Sequence ID - 600                    nt:     595
Length=595


   SEQ ID NO: 206                 nt:     595

ALIGNMENTS
 Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query  1    TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTATAGCC  60

Query  61   TTTCCAATTTTCTTTCGCTTGGAttttacgtgataagttttttcccccattttacttta  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTCCAATTTTCTTTCGCTTGGATTTTACGTGATAAGTTTTTTCCCCCATTTTACTTTTA  120

Query  121  ncaactctatattttttaGTTGAGGTTGGGTTTCTTGTAAACAGCATATAATTTGGGTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  NCAACTCTATATTTTTTAGTTGAGGTTGGGTTTCTTGTAAACAGCATATAATTTGGGTTT  180

Query  181  TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTTACACATAATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATACCATTTACACATAATG  240

Query  241  TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAAtt  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCTAGTTGTGCTCTACTTGAATT  300

Query  301  tttttttAGTATTCTGTTTTAATTGACCACATTTGACTGTATCTCTTTGTGTAATTCTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTTTTAGTATTCTGTTTTAATTGACCAACATTTGACTGTATCTCTTTGTGTAATTCTT  360

Query  361  TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTACAGGTTGCTGTAGGCATGACAATATATACACTTAACTTTTCTCAGTACACTGAGAGT  420

Query  421  TGAAATTGTAGTACTTCGAGGAAAACATAGAAAACTTGCAATGATATCGGTTACATTTTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAAATTGTAGTACTTCGAGGAAAACATAGAAAACTTGCAATGATATCGGTTACATTTTA  480
```

```
Query  481  CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCACCTCCATATGTTGCAATTATTAAATGTATTAGATCTGCCTACCTCGAAAACCCATCA  540

Query  541  GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTTaaaaaaaCTTGAGGCAA  595
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTCTTTTAACTTTGCTCTCAATGGTGATTCATATTTTTAAAAAAACTTGAGGCAA  595
```

# Sequence 601 matched with Sequence 207

```
Query=   Sequence ID - 601                    nt:     522
Length=522


   SEQ ID NO: 207                  nt:     522

ALIGNMENTS
 Identities = 522/522 (100%), Gaps = 0/522 (0%)

Query  1    TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTACATTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTACATTT  60

Query  61   CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTTCTTTAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTTTTCTTTAG  120

Query  121  CAAGAATTAAGGATTTTGGTGGGTGGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAAGAATTAAGGATTTTGGTGGGTGGGGGGAGGCTTCTGTGGGGACCAAGACAATGTACT  180

Query  181  GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGAGAACAGTTGATCGTGT  240

Query  241  TTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTGCATTGCAGCTTCCGATAGAG  300

Query  301  CTTTTTATTTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTTTTATTTTTGGATATCAGGAACCAATTTTGAAGATTTCTTAAGAAAGTCATTTACAT  360

Query  361  CAGGGACATGAAGAGCAAAGTAGGTATTTTTGGTCAGTACTTGAATTTGATAGGCTTTAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAGGGACATGAAGAGCAAAGTAGGTATTTTTGGTCAGTACTTGAATTTGATAGGCTTTAT  420

Query  421  GCAAACAACTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCAAACAACTCTCCCTCTGCTGGAGTCTGGCAAGTTTGCTTTTCACTGGACGCTAATTCA  480
```

```
Query  481   AGTGCCATACAAAACTAAAATAANAGTTTTACTTATAACACA   522
             ||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGTGCCATACAAAACTAAAATAANAGTTTTACTTATAACACA   522
```

# Sequence 602 matched with Sequence 208

Query=  Sequence ID 602
Length=585


   SEQ ID NO: 208

ALIGNMENTS
 Identities = 585/585 (100%), Gaps = 0/585 (0%)

```
Query  1    CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACTACCT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACTACCT   60

Query  61   TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAGGGAGTGTA   120

Query  121  TAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCCATGGTTCAGCTG   180

Query  181  TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTTGACAGTGCCAAATCAA   240

Query  241  AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGGGGACTTCCAGCTACACACTA   300

Query  301  ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGTCAATGATGGGACAGAATTTGGAGGATCAATTTATCAGAAAGTTTGTGAAGATCTTG   360

Query  361  ACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACACTTCAGTAAACCTTGCTTGGACATCAGGTACCAACTGCACTCGTTTTGGCATTGCAG   420

Query  421  CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTAAATATCAGTTGGATCCCACTGCTTCCATTTCTGCAAAAGTCAACAACTCTAGCTTAA   480
```

```
Query  481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGGAGTAGGCTATACTCAGACTCTGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGG  540

Query  541  TAGATGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGGCTCG  585
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAGATGGGAAGAGCATTAATGCTGGAGGCCACAAGGTTGGGCTCG  585
```

# Sequence 603 matched with Sequence 209

```
Query=  Sequence ID - 603                    nt:    624
Length=624


   SEQ ID NO: 209                 nt:    624

ALIGNMENTS
 Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query  1    GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA  60

Query  61   GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC  120

Query  121  TGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCA  180

Query  181  AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT  240

Query  241  GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA  300

Query  301  TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC  360

Query  361  GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT  420

Query  421  TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC  480
```

```
Query  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540

Query  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600

Query  601  CCACCCTACCACACATTCGAAGAA  624
            ||||||||||||||||||||||||
Sbjct  601  CCACCCTACCACACATTCGAAGAA  624
```

# Sequence 605 matched with Sequence 210

```
Query=  Sequence ID - 605              nt:     338
Length=338


   SEQ ID NO: 210              nt:     338

ALIGNMENTS
 Identities = 338/338 (100%), Gaps = 0/338 (0%)

Query  1    ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCCTAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCCTAAT  60

Query  61   ACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTCCTCCAGCA  120

Query  121  GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTTCAGTCAGCGCAA  180

Query  181  GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAATCTTTA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATGAATATATAAATCTTTA  240

Query  241  TACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTATGGAAACTTGGCAGAGCCAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTATGGAAACTTGGCAGAGCCAG  300

Query  301  AGTGTACACATTCCTAAACCATTAAACAGATTTCTATA    338
            ||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGTGTACACATTCCTAAACCATTAAACAGATTTCTATA    338
```

## Sequence 606 matched with Sequence 211

```
Query=   Sequence ID - 606                    nt:      556
Length=556


   SEQ ID NO: 211                 nt:      556

ALIGNMENTS
 Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query   1    GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTGCATG   60

Query   61   AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACAAGGCAGGA   120

Query   121  AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAACTGGATGTTTGCT   180

Query   181  AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCCAGAAACCTGGAGAGA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCCCAGAAACCTGGAGAGA   240

Query   241  TTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACC   300

Query   301  ATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATATTTCATGTGCATGAAAGCCCTAGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATATTTCATGTGCATGAAAGCCCTAGA   360

Query   361  ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTA   420

Query   421  GGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATAT   480
```

```
Query   481   AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AGTATACTGAAAGTGAACAGATCTTTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGT   540

Query   541   GTCTGCCGGACAGTGC   556
              ||||||||||||||||
Sbjct   541   GTCTGCCGGACAGTGC   556
```

# Sequence 607 matched with Sequence 212

```
Query=   Sequence ID 607
Length=305


   SEQ ID NO: 212

ALIGNMENTS
 Identities = 305/305 (100%), Gaps = 0/305 (0%)

Query  1    CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATTTCTT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATTTCTT   60

Query  61   TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAAAATGCCAT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAAAATGCCAT   120

Query  121  GGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATATGCTTATAACACT   180

Query  181  AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTTGCATTCCAAT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATATTTGTTTGCATTCCAAT   240

Query  241  TTTGTTTAATAATGAGTGTGTAAACTGCATACGTTAAATAAATGTAAATACTAATGTACT   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTGTTTAATAATGAGTGTGTAAACTGCATACGTTAAATAAATGTAAATACTAATGTACT   300

Query  301  GCTGC   305
            |||||
Sbjct  301  GCTGC   305
```

# Sequence 609 matched with Sequence 213

Query=   Sequence ID 609
Length=495


   SEQ ID NO: 213

ALIGNMENTS
 Identities = 495/495 (100%), Gaps = 0/495 (0%)

```
Query  1    TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATtttgttgttgttgttgttgtngttgt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATTTGTTGTTGTTGTTGTTGTNGTTGT  60

Query  61   tgttgAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTTGAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAGGAAGTAGT  120

Query  121  CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGTCTATTGTAACTT  180

Query  181  CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTCTAAATGGTCATGAAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTCTAAATGGTCATGAAAA  240

Query  241  GAAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGGACTATTATGTCTTTTAGATT  300

Query  301  TCCTGTGGGTTTCTAGGAATGTTAGTGTAACTTANATTTCCACCTACCTGATTTCTGGAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCTGTGGGTTTCTAGGAATGTTAGTGTAACTTANATTTCCACCTACCTGATTTCTGGAT  360

Query  361  GTGCCTATTGGAACTTGCTGAGATCtttttttttCCTTAACATGTTGTCCCCTTGACCCG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTGCCTATTGGAACTTGCTGAGATCTTTTTTTTTCCTTAACATGTTGTCCCCTTGACCCG  420

Query  421  TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACTTCGAAACTAAACATATTATTTTATTTGCTTACACTTCAGGAGGCAATTGGCAGACA  480
```

```
Query  481   CCAGGCCAACAGTCT   495
             |||||||||||||||
Sbjct  481   CCAGGCCAACAGTCT   495
```

# Sequence 610 matched with Sequence 214

Query=   Sequence ID 610
Length=507


   SEQ ID NO: 214

ALIGNMENTS
 Identities = 507/507 (100%), Gaps = 0/507 (0%)

```
Query  1    GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACCATTT  60

Query  61   ATGACATTGCTTGGTGTCAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGACATTGCTTGGTGTCAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGATGACGCGA  120

Query  121  TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCCACCTTCTCCCTGACAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCCACCTTCTCCCTGACAG  180

Query  181  CCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCCTGGAACCCCAAGGAGC  240

Query  241  CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGCCTTCTGGAAGTATCAGCGGC  300

Query  301  CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAGTAATGACTCCCCAGAAAACGTCAT  360

Query  361  ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTTAACTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATAAGACTTTACCAGCCCCTGAGAGGACCAGGAGGAGCATCCTTGACCTTCATTTAACTT  420

Query  421  GGCTCACTTCTCTTCANACTTGGGTAGAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCTCACTTCTCTTCANACTTGGGTAGAAGTGCAGAGCCACAAAATTGCTTTCCTTCCCC  480
```

```
Query  481  GCCTTTGACATGAGGCCTTCAGTAAAG  507
            |||||||||||||||||||||||||||
Sbjct  481  GCCTTTGACATGAGGCCTTCAGTAAAG  507
```

# Sequence 611 matched with Sequence 215

BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

Query=   Sequence ID 611
Length=17

   SEQ ID NO: 215                                      34.2    1e-08

ALIGNMENTS
 Identities = 17/17 (100%), Gaps = 0/17 (0%)

Query  1    TGCAGGATCCGTCGACT  17
            |||||||||||||||||
Sbjct  1    TGCAGGATCCGTCGACT  17

# Sequence 612 matched with Sequence 216

Query=   Sequence ID - 612                    nt:      576
Length=576


   SEQ ID NO: 216                 nt:     576

ALIGNMENTS
 Identities = 576/576 (100%), Gaps = 0/576 (0%)

```
Query  1    GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCCTGAAAGAGATG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCCTGAAAGAGATG  60

Query  61   AGGAGAATGGGACAAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGAGAATGGGACAAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAACTTCCCCA  120

Query  121  ATCTTGCTAGAGAGGCCAACATTAAAATTCAGTAAATGCTGAAAACTCCAGTAAGATATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATCTTGCTAGAGAGGCCAACATTAAAATTCAGTAAATGCTGAAAACTCCAGTAAGATATT  180

Query  181  TCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCTAAGGTCAAATGAAGGA  240

Query  241  AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACCTACAAAGAGAATGGCATAAG  300

Query  301  ACAAAAAGTAGAACTCCCAGCAGAAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACAAAAAGTAGAACTCCCAGCAGAAACTCTAAAAGCCAGAAGAGATTAGGGGCCAATATT  360

Query  361  TAACATTCTGAAAGAAATTCCAACAAGGAATTTCATATCCAGCCAAACTAAGCTTCATAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAACATTCTGAAAGAAATTCCAACAAGGAATTTCATATCCAGCCAAACTAAGCTTCATAA  420

Query  421  TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTGAAGGAGAAATAAGATATTTTCCAGACAAGCAAATGCTGATGAAATCCATCACCACCA  480
```

```
Query  481   GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GACCTGCCTTATAAGAGCTCCTGAGGGAAGCACTAAATATTGAAAGGGAAGAACTTTATG   540

Query  541   AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG   576
             ||||||||||||||||||||||||||||||||||||
Sbjct  541   AACCATTTCAAAAACACATTTAAGTNCACAAAGCAG   576
```

# Sequence 613 matched with Sequence 217

```
Query=   Sequence ID - 613                    nt:      341
Length=341


   SEQ ID NO: 217                 nt:     341

ALIGNMENTS
 Identities = 341/341 (100%), Gaps = 0/341 (0%)

Query  1    CCTTATTTTACAGGTGAAAAACCACGAATCAGATAGATTTTTATTTGCCCAAGTCACATA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCTTATTTTACAGGTGAAAAACCACGAATCAGATAGATTTTTATTTGCCCAAGTCACATA  60

Query  61   ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTTGGGAGGCT  120

Query  121  AAGGCGGGTGGATTTCCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGGCGGGTGGATTTCCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAAC  180

Query  181  CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGAGAGCCTGTAGTCCTGG  240

Query  241  CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGGGAAGTCGAGGCTGCAGTGGC  300

Query  301  AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT   341
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACAGAATGGGTAACCTGGACATCAGAGTGAGACCCTGTCT   341
```

# Sequence 614 matched with Sequence 218

Query=  Sequence ID 614
Length=494


   SEQ ID NO: 218

ALIGNMENTS
 Identities = 494/494 (100%), Gaps = 0/494 (0%)

```
Query  1    CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCCCAGG  60

Query  61   AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGAAATAGCCA  120

Query  121  GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGTGGAAGGCTGCCT  180

Query  181  TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCACTGCACTCCAACCTGGG  240

Query  241  AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAATAGGCCAGGCACAGTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCCAAAATAGGCCAGGCACAGTG  300

Query  301  ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCCGGATCATTTGAGGTCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAAATAGGCCGGATCATTTGAGGTCAG  360

Query  361  GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAAACCACATCTCTACTACAAATAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGTTCAAATTCAAGACCAGCCCGGCCAACATGGCAAAACCACATCTCTACTACAAATAA  420

Query  421  AAAATTAGTTGGGTGTGGNGGAGCATTCCTGTAATCACAGCTATTCAGGAGGCTGAGGCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAATTAGTTGGGTGTGGNGGAGCATTCCTGTAATCACAGCTATTCAGGAGGCTGAGGCA  480
```

```
Query  481  TGANAACCGCTTCA  494
            ||||||||||||||
Sbjct  481  TGANAACCGCTTCA  494
```

## Sequence 615 matched with Sequence 219

```
Query=  Sequence ID - 615              nt:     379
Length=379


   SEQ ID NO: 219              nt:     379

ALIGNMENTS
 Identities = 379/379 (100%), Gaps = 0/379 (0%)

Query  1    TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCTACTT  60

Query  61   GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTGAGCTGTGA  120

Query  121  TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTaaaaaataaaaa  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCTAAAAAATAAAAA  180

Query  181  aTACAAATACAACTACAAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATACAAATACAACTACAAACTAGCACTAGACCAACAGTGACTATGTACCATGAACTGAGG  240

Query  241  AATATTATTAATTCCACCATTTGCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATATTATTAATTCCACCATTTGCATCTGAGGTTAACAATATGTCAATGACTTAAATAAC  300

Query  301  ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATCATATCTCTGAGAGTAATTTCTCCTATATTTCCATGACAAATGTTAGATAATTTTCCA  360

Query  361  TTTTTTCCATTCAACAAAA  379
            |||||||||||||||||||
Sbjct  361  TTTTTTCCATTCAACAAAA  379
```

## Sequence 617 matched with Sequence 220

```
Query=   Sequence ID 617
Length=421


   SEQ ID NO: 220


ALIGNMENTS
 Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query  1    TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCCTGAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCCTGAC  60

Query  61   ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCGCATACCCG  120

Query  121  AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCGGTACTAAGTCATTTTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCGGTACTAAGTCATTTTC  180

Query  181  AGGGGATTGAAAGACTATTGCTGGATTTCATGATGCTGACTGGCGTTAGCTGATTAACCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGGGATTGAAAGACTATTGCTGGATTTCATGATGCTGACTGGCGTTAGCTGATTAACCC  240

Query  241  ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACAAAGACTGGCTTCTGGACTTC  300

Query  301  CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTCCCTGATCCCCACTCTTACTCATCACCTGCAGTGGCCAGAATTAGGGACTCAGAATCA  360

Query  361  AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AACCAGTGTAAGGCAGTGCTGGCTGCCATTGCCTGGTCACATTGAAATTGGTGGCTTCAT  420

Query  421  T  421
            |
Sbjct  421  T  421
```

# Sequence 618 matched with Sequence 221

```
Query=   Sequence ID - 618                    nt:     598
Length=598


   SEQ ID NO: 221                 nt:     598

ALIGNMENTS
 Identities = 598/598 (100%), Gaps = 0/598 (0%)

Query  1     GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATTTTGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATTTTGC  60

Query  61    GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTAATTTACTC  120

Query  121   CTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGAGGAAATTAAGAC  180

Query  181   CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAGGGCCAGAACTTTGCCT  240

Query  241   CAGAGAATCTGAATTTCCAAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CAGAGAATCTGAATTTCCAAAAAATAACCTAAAAGAGAAATTTAAGTACTAATTAGTAAG  300

Query  301   CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CAAAGAAATGCACATTTAAGGAAGACAGTGCACATTTAAGGAAGACAGTAACCTTTTATC  360

Query  361   TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TATTAGAGAAAAACACACATTCTGTCTTTAACACACACATAAATCTTATATTGGCAGGGA  420

Query  421   TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TTTTCTTTATTCAGCAATTATTTATTGGTTGTCTGCTTTGTGGTACACATAAATGCTGGG  480
```

```
Query  481  GATAAACACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GATAAACACTTAATAAAATATACTTCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAG  540

Query  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTAAGTCAACAGAGTAGAGGTGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG  598
```

# Sequence 619 matched with Sequence 222

Query=  Sequence ID 619
Length=473


   SEQ ID NO: 222

ALIGNMENTS
 Identities = 473/473 (100%), Gaps = 0/473 (0%)

```
Query  1    GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGGATCA  60

Query  61   GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCATGTGGGTTG  120

Query  121  TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACAGCCCCAAAGGAA  180

Query  181  TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGACTTTGGCAAAAGGATGT  240

Query  241  TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTTCTTCCAGGCAGCCTTCCTGG  300

Query  301  AGGAGAGAGATGCCTGGGTTCGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGGAGAGAGATGCCTGGGTTCGGGATATCAATAAGGCCATTAAATGCATTGAAGGAGGCC  360

Query  361  AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTCGACTGCCAGAAACCATTGACTTAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGAAATTTGCCAGGAAATCTACCAGGAGGTCCATTCGACTGCCAGAAACCATTGACTTAG  420

Query  421  GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT    473
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGCCTTATATTTGTCCATGAAAGACACTGAAAAAGGAATAAAAGAACTGAAT    473
```

## Sequence 621 matched with Sequence 223

Query= Sequence ID 621
Length=392


SEQ ID NO: 223

ALIGNMENTS
 Identities = 392/392 (100%), Gaps = 0/392 (0%)

```
Query  1    TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACATACTT  60

Query  61   CCCCCATTATTCCTAGAACCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCCCCATTATTCCTAGAACCAGGCGACCTGCGACTCCTTGACGTTGACAATCGAGTAGTA  120

Query  121  CTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTCTTGCACTCATGA  180

Query  181  GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACGTCTAAACCAAACCACT  240

Query  241  TTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCTCTGAAATCTGTGGAGCAAAC  300

Query  301  CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCCCTAAAAATCTTTGAAATAGGGCCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACAGTTTCATGCCCATCGTCCTAGAATTAATTCCCCTAAAAATCTTTGAAATAGGGCCC  360

Query  361  GTATTTACCCTATAGCACCCCCTCTACCCCCT  392
            ||||||||||||||||||||||||||||||||
Sbjct  361  GTATTTACCCTATAGCACCCCCTCTACCCCCT  392
```

# Sequence 622 matched with Sequence 224

Query=  Sequence ID 622
Length=618


   SEQ ID NO: 224

ALIGNMENTS
 Identities = 618/618 (100%), Gaps = 0/618 (0%)

```
Query  1    TTTTTCTTGTTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTCTTGTTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCATTTA  60

Query  61   TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAAGATTGAGA  120

Query  121  GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAGATAAAGATCATA  180

Query  181  TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAAATATGTTTTTATTGTT  240

Query  241  TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTTGAGAATGCATTGTGTTTGGT  300

Query  301  ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCaataata  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACTGTTTTTTATGAATATCATTAAAAATTTATTTAAGGAGAGAGTAATTTTGCAATAATA  360

Query  361  tttttgatttatttgaaaataaaattcaagataaatgaaataattgaaattttCTAAAGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTTTGATTTATTTGAAAATAAAATTCAAGATAAATGAAATAATTGAAATTTTCTAAAGA  420

Query  421  AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAACTGAACCATTTATATAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGGAATTGAATATATTTTTACATTTGAATGAACTAAGGATTAACTGAACCATTTATATAT  480
```

```
Query  481  AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTACTTTCAGAACTGAATGTCTTAAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCT  540

Query  541  TTCAAGTCAAAGAACCCAGAAACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTCAAGTCAAAGAACCCAGAAACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGG  600

Query  601  ATTAGTGAGTATAAATTT  618
            ||||||||||||||||||
Sbjct  601  ATTAGTGAGTATAAATTT  618
```

# Sequence 624 matched with Sequence 225

BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

Query=   Sequence ID 624
Length=17

```
   SEQ ID NO: 225                                      34.2    1e-08

ALIGNMENTS
 Identities = 17/17 (100%), Gaps = 0/17 (0%)

Query  1    TGCAGGATCCGTCGACT  17
            |||||||||||||||||
Sbjct  1    TGCAGGATCCGTCGACT  17
```

# Sequence 625 matched with Sequence 226

Query=   Sequence ID 625
Length=396


   SEQ ID NO: 226

ALIGNMENTS
 Identities = 396/396 (100%), Gaps = 0/396 (0%)

```
Query  1    GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGCCTGA  60

Query  61   GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATGAGGCTTTG  120

Query  121  GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCCTGGTGGTTCTGCACGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCCTGGTGGTTCTGCACGT  180

Query  181  TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGaaaaaataaaaaaTCCAAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGAAAAAAATAAAAAATCCAAAGA  240

Query  241  CCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAATGCCTATTTGGTGCTCATAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAATGCCTATTTGGTGCTCATAA  300

Query  301  AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGATTAATCATGTCACGCATGTTTCCAATCTTTCTTTTGCAGTATATTATTTTCTAAAAA  360

Query  361  TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA  396
            ||||||||||||||||||||||||||||||||||||
Sbjct  361  TTGTTACATGCAAATTTAAACCAAGATTTATCAGTA  396
```

# Sequence 626 matched with Sequence 227

Query=  Sequence ID 626
Length=535


   SEQ ID NO: 227

ALIGNMENTS
 Identities = 535/535 (100%), Gaps = 0/535 (0%)

```
Query  1    TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTGCTAA   60

Query  61   CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG   120
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  61   CTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACNCCACAAAG   120

Query  121  ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGCAGCCTCCTTAAG   180

Query  181  TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAACAGAGCAGATTGTCAA   240

Query  241  TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNTAAGCTGCTTGGTTGGCCTTA   300

Query  301  AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGTGCCGACAATTAAGAGATGAAGGCAATGAGAACTGAAACAAACATTTAAGTTCAAGAC   360

Query  361  CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCAGTTTACTGACACTGGGACTATTACTATATCTCTTTGGGCCTCAGTTTACTTATCTGT   420

Query  421  AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCtttttttttATTTAGAGATGGG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AACATTAAGAGGTTGGATTACATGATGTCTCACGATTCTTTTTTTTTTATTTAGAGATGGG   480
```

```
Query  481  GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG  535
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCATAGCTCACAGCAG  535
```

# Sequence 627 matched with Sequence 228

```
Query=   Sequence ID 627
Length=392


   SEQ ID NO: 228

ALIGNMENTS
 Identities = 392/392 (100%), Gaps = 0/392 (0%)

Query  1    CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTAACTC  60

Query  61   TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGCCTCCGCAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGCCTCCGCAT  120

Query  121  CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTCGGGCCTACACTG  180

Query  181  TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGTGTTCAAGGCAGACTTC  240

Query  241  CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCAGTGTGAGCCCCAAGGGCAAG  300

Query  301  AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTaaaaaaaaG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  301  AACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCCATCTGGATGGAAGGTAAAAAAAAG  360

Query  361  AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT  392
            ||||||||||||||||||||||||||||||||
Sbjct  361  AAAATCCCTTGAAAGGAGATTGAGGGAAGTTT  392
```

## Sequence 628 matched with Sequence 229

```
Query=  Sequence ID - 628                    nt:    419
Length=419


   SEQ ID NO: 229                 nt:    419

ALIGNMENTS
 Identities = 419/419 (100%), Gaps = 0/419 (0%)

Query  1    AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGTAGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGTAGAA  60

Query  61   TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACATATGAGAA  120

Query  121  TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATTGTCTACTCCTAG  180

Query  181  AAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATCCTGTAAATATATCTTA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATCCTGTAAATATATCTTA  240

Query  241  AGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTTGGGttttttttttAGTTGCCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTTGGGTTTTTTTTTTAGTTGCCA  300

Query  301  ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTCTAAGAAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACAGTTGTATGTTTGCTGATTATTTATGACCTGAAATAATATATTTCTTCTTCTAAGAAG  360

Query  361  ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTT  419
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACATTTTGTTACATAAGGATGACTTTTTTATACAATGGGAATAAATTATGGCATTTTTT  419
```

## Sequence 629 matched with Sequence 230

```
Query=   Sequence ID 629
Length=622


   SEQ ID NO: 230

ALIGNMENTS
 Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query  1    CTGAGAGTCACTGTGTTTTTAGCCAAATCTAAGGGAGAAAATGAATATTGATAGCAGCAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGAGAGTCACTGTGTTTTTAGCCAAATCTAAGGGAGAAAATGAATATTGATAGCAGCAT  60

Query  61   GCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTTAGTGCTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTTAGTGCTTC  120

Query  121  AGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCATGCATTGACCAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCATGCATTGACCAAT  180

Query  181  TTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTtatatatatatatttttttagtt  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTTATATATATATATTTTTTTAGTT  240

Query  241  tttttAATGTAAATGAGAGAATAAAGatatatatatatgtctatatatgtatatatgtat  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTTTAATGTAAATGAGAGAATAAAGATATATATATATGTCTATATATGTATATATGTAT  300

Query  301  atatatgtctatatgtctatatgtatatatgtctatatgtatatatgtgtgtgtgtatat  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATATATGTCTATATGTCTATATGTATATATGTCTATATGTATATATGTGTGTGTGTATAT  360

Query  361  atatatatatatataAGTTTTCTGTTGCTAGCATAACAAACTACCAGAAACTTAGCAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATATATATATATATAAGTTTTCTGTTGCTAGCATAACAAACTACCAGAAACTTAGCAA  420

Query  421  CTGAAACAACATGAATTTATCTTACGGTTCTATAGTTCAGAAGTCTAACGTGTCACTGGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTGAAACAACATGAATTTATCTTACGGTTCTATAGTTCAGAAGTCTAACGTGTCACTGGG  480
```

```
Query  481  ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATTCAGCTACCTGGCTCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGAAATCCAGGTTTCAACAGGACTGGGTTCCCTTCTAGCTCATTCAGCTACCTGGCTCA  540

Query  541  TTCAGGTTGTNGGCAGAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTCAGGTTGTNGGCAGAATATACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCC  600

Query  601  TGGCTATCATCTGAAAACTTTC  622
            ||||||||||||||||||||||
Sbjct  601  TGGCTATCATCTGAAAACTTTC  622
```

# Sequence 630 matched with Sequence 231

Query=  Sequence ID 630
Length=350


   SEQ ID NO: 231

ALIGNMENTS
 Identities = 350/350 (100%), Gaps = 0/350 (0%)

```
Query  1    AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTACGTGC  60

Query  61   CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATCCATCCAGA  120

Query  121  TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAAAACTTATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGTTTAAAACTTATG  180

Query  181  CTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCCATTCTCCGATTGGCCA  240

Query  241  AGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGTGGAATATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAGAATCACAGATGTGGAATATT  300

Query  301  TGTCATAAATAAATAATGAAAACCTaaaaaaaaaaaaaaaaaaaaaaaaa   350
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGTCATAAATAAATAATGAAAACCTAAAAAAAAAAAAAAAAAAAAAAAAA   350
```

# Sequence 631 matched with Sequence 232

Query=  Sequence ID 631
Length=493


   SEQ ID NO: 232

ALIGNMENTS
 Identities = 493/493 (100%), Gaps = 0/493 (0%)

```
Query  1    TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG  62
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATGGGCCAG  62

Query  63   CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT  122
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   CCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAGCTCCCTACAT  122

Query  123  AGTTACTTGTAAACTCCTCCTCTCTGTATAAGTTTTCCTGAAttttttttGATAAAATTAA  182
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  AGTTACTTGTAAACTCCTCCTCTCTGTATAAGTTTTCCTGAATTTTTTTGATAAAATTAA  182

Query  183  GTTGTGCCACCCCTTTATGCTCTCTTANAACTTTGTTCTGTTCTCATGGCTGTTCTGCAA  242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  GTTGTGCCACCCCTTTATGCTCTCTTANAACTTTGTTCTGTTCTCATGGCTGTTCTGCAA  242

Query  243  CGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTGCGTCTCCCACTAGATGGCAGAC  302
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  CGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTGCGTCTCCCACTAGATGGCAGAC  302

Query  303  TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGCAGAAAGCCTG  362
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303  TCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTGGATCCCTGGCACTTGCAGAAAGCCTG  362

Query  363  TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTTAAAACGCCAA  422
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363  TTACGTAATAATTGCTCAACAATTAGTTTTTAAATAAATGAATTATTTTTAAAACGCCAA  422

Query  423  AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC  482
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423  AATTACAATGATTGTGCATTAAGTGAAAGATGACCATCTAAAAACATAAAGCCATGCTTC  482
```

```
Query  483  ATGACATTGGC  493
            |||||||||||
Sbjct  483  ATGACATTGGC  493
```

Blast comparison trimmed "TN" from the 5' end of both sequences and reported 491 identities. The report has been manually corrected for this. "TN" has been prepended to both sequences and identity count has been increased to 493.

# Sequence 632 matched with Sequence 233

Query=  Sequence ID 632
Length=577


   SEQ ID NO: 233

ALIGNMENTS
 Identities = 577/577 (100%), Gaps = 0/577 (0%)

```
Query  1    GACCATTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCATTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAATGCCG  60

Query  61   ATGAGGTGGATGCAATTTCCTTTTGTGCAAGCAGTGCACGGTGcccccccCTCGGGTGTC  120
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  61   ATGAGGTGGATGCAATTTCCTTTTGTGCAAGCAGTGCACGGTGCCCCCCCCCTCGGGTGTC  120

Query  121  CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGGGGCTGGGCAAGG  180

Query  181  CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCCCTGTTACAGGTGGTCA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCCCTGTTACAGGTGGTCA  240

Query  241  AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAATATCCTCTGCCCCTGGGTGGT  300

Query  301  TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCCATGGGA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGTTTGGCGAAAGCCCGCCCCATGGGA  360

Query  361  TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCCACCCCTGTGGGAC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTGAGGGACGGGGCTGCACTCCAACCGTCTGCACCTGCTCTTCCCCCACCCCTGTGGGAC  420

Query  421  CTCATCTTCACGTGCCATGTGTGCTGAAGGCCCAGGGCCCAGCAGGGGGCAGTGGCACCT  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTCATCTTCACGTGCCATGTGTGCTGAAGGCCCAGGGCCCAGCAGGGGGCAGTGGCACCT  480
```

```
Query  481   GTTGACGGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GTTGACGGAAAAGCCGAGGTGCTTACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTT   540

Query  541   GTCGGGCATTCAGGGCCCCGACCTGTGCCTACCCGCA   577
             |||||||||||||||||||||||||||||||||||||
Sbjct  541   GTCGGGCATTCAGGGCCCCGACCTGTGCCTACCCGCA   577
```

# Sequence 633 matched with Sequence 234

Query=   Sequence ID 633
Length=568


   SEQ ID NO: 234

ALIGNMENTS
 Identities = 568/568 (100%), Gaps = 0/568 (0%)

```
Query   1    CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA   60

Query   61   GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCT   120

Query   121  GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCT   180

Query   181  GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGTGCT   240

Query   241  CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  CGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCACACT   300

Query   301  GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGGCAA   360

Query   361  CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCCACCAGTGCAGGC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCCACCAGTGCAGGC   420

Query   421  TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TGCCTATCANAAAGTGGTGGCTGGTGTGGGCTAATGCCTGGCCCCACAAGTATCACTAAG   480
```

```
Query  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACT  540

Query  541  AAACTGGGGGATATTATGAAGGGCCTTG  568
            ||||||||||||||||||||||||||||
Sbjct  541  AAACTGGGGGATATTATGAAGGGCCTTG  568
```

# Sequence 634 matched with Sequence 235

```
Query=   Sequence ID - 634                     nt:     511
Length=511


   SEQ ID NO: 235                    nt:     511

ALIGNMENTS
 Identities = 511/511 (100%), Gaps = 0/511 (0%)

Query  1    TTTTTTAATTTCACCAAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATAATTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTAATTTCACCAAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATAATTA  60

Query  61   AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGATGTTGACT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGATGTTGACT  120

Query  121  TAGCACCTTCTCTCtttttttttttttttttttGAGTTGGAGTCTTGCTCTGTCACCCAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGCACCTTCTCTCTTTTTTTTTTTTTTTTTTTGAGTTGGAGTCTTGCTCTGTCACCCAG  180

Query  181  CTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCGGGCGCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCGGGCGCT  240

Query  241  TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTGCATGCCGCCACNCCTAGCTA  300

Query  301  ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGTTTTTTGTATCTTGGTANANATGGNGTTTCACCTTGTTGCCCATGCCGCTCTTGAAC  360

Query  361  TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCCTTGGCCTCCCAAAGTGTTAGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAATTT  420

Query  421  ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ANCACCTTACTGGGTGCTGAGGCTGTGAGCCATAGTAGAATGCATGTGATCCAGGGCCTT  480
```

```
Query  481  GCTGAATTCATGGGCTAATAGGGAGCCTGAC  511
            |||||||||||||||||||||||||||||||
Sbjct  481  GCTGAATTCATGGGCTAATAGGGAGCCTGAC  511
```

# Sequence 635 matched with Sequence 236

```
Query=  Sequence ID - 635                    nt:    592
Length=592


    SEQ ID NO: 236                 nt:    592

ALIGNMENTS
 Identities = 592/592 (100%), Gaps = 0/592 (0%)

Query  1    TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCCAGAGCCATGCCCGAGATAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCCAGAGCCATGCCCGAGATAGT  60

Query  61   GGATACCTGTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGATACCTGTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTGCACCTGCG  120

Query  121  CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCTCACGGTCCAGTC  180

Query  181  TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACCTTACAATAGAAAAAGT  240

Query  241  AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAAAGACAAAGTTACAAGGGATC  300

Query  301  GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAAAAATCAAGAAATTGTTATAGAAAT  360

Query  361  TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCTTTTGAGACCTCTCCAAAATCTTCTGCTCTCCAGTGGCTCACTCCTGAACAGACTTC  420

Query  421  TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGGAAGGAACACCCATATCTCTTTAGTCAGTGCCAGGCCATCCACTGCAGAGCAATCCT  480
```

```
Query  481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCCTTGTCAGGACACTCCTTCTGNGAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAA  540

Query  541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGAACTGGTGGCACTTATGAGTGCTATTCGTGATGGAGAAACACCTGACCCA  592
```

## Sequence 636 matched with Sequence 237

```
Query=  Sequence ID - 636                      nt:     572
Length=572


   SEQ ID NO: 237                  nt:     572

ALIGNMENTS
 Identities = 572/572 (100%), Gaps = 0/572 (0%)

Query  1    CTTANAAGAGTTGCTCATTCACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGAGCGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTANAAGAGTTGCTCATTCACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGAGCGA  60

Query  61   AACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCCATGTTGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCCATGTTGAA  120

Query  121  GAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCCACCCAGAACACTTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCCACCCAGAACACTTC  180

Query  181  TTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCAAGTGGCTGTTCTCCAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCAAGTGGCTGTTCTCCAA  240

Query  241  CTTTCCCAAGCCGCTTGCATTCCCCAGACTGGACTACTGTGGCGGTTAGGTTAGATTTGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTTCCCAAGCCGCTTGCATTCCCCAGACTGGACTACTGTGGCGGTTAGGTTAGATTTGA  300

Query  301  AGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCCCTCTTCTCCTCTTccccccACAT  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct  301  AGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCCCTCTTCTCCTCTTCCCCCCCACAT  360

Query  361  CTCTCATGAGAGAGGTAGTGGCATTTCCTTCTCAGGGAGCTTCAATGGGAAAGGTCTCGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCTCATGAGAGAGGTAGTGGCATTTCCTTCTCAGGGAGCTTCAATGGGAAAGGTCTCGA  420

Query  421  AAGCTTCAGGAGGAGCAGAATACCAACGCAGGGGGATGGCTGTAACGATCTCACCGTCTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGCTTCAGGAGGAGCAGAATACCAACGCAGGGGGATGGCTGTAACGATCTCACCGTCTC  480
```

```
Query  481  CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTAACCTCAGTCCCTTTTTTGAGAGTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTG  540

Query  541  TAGATCTCTTTGTCTGGGGGAGGGGAANGATG  572
            |||||||||||||||||||||||||||||||
Sbjct  541  TAGATCTCTTTGTCTGGGGGAGGGGAANGATG  572
```

## Sequence 637 matched with Sequence 238

```
Query=  Sequence ID - 637                    nt:    482
Length=482


   SEQ ID NO: 238                nt:    482

ALIGNMENTS
 Identities = 482/482 (100%), Gaps = 0/482 (0%)

Query  1    TTAAAACAGGCGCAGGGGTAAAAATGAGAATGAATCTGAAAAAAGAGAGTTGGTGTTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTAAAACAGGCGCAGGGGTAAAAATGAGAATGAATCTGAAAAAAGAGAGTTGGTGTTTAA  60

Query  61   AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGATTGGAAGC  120

Query  121  ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATTGAGAAAAAAGGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATTGAGAAAAAAGGT  180

Query  181  TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACTATCAGGATAACAAAGC  240

Query  241  TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGCCTGAAGGCATATGGCGAGCT  300

Query  301  TCCAGAACATGCTAAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCAGAACATGCTAAAATCAATGAAACAGACACATTTGGTCCTGGAGATGATGATGAAAT  360

Query  361  CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCAGTTTGACGATATTGGAGATGATGATGAAGACATTGATGATATCTAAATTGAACCAAG  420

Query  421  TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTTTTTACATGACAAGTTCTCTGAGGATGGTTCTACAGTTGGGATTTTGGCCATCATCA  480
```

```
Query  481  AC  482
            ||
Sbjct  481  AC  482
```

## Sequence 638 matched with Sequence 239

```
Query=  Sequence ID - 638                    nt:     545
Length=545


   SEQ ID NO: 239                 nt:     545

ALIGNMENTS
 Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query  1    TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGATAAG  60

Query  61   AAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAATTTAAGGGAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAATTTAAGGGAAAA  120

Query  121  ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACACAGCCTAGGACA  180

Query  181  GTACCTGCACATAGTAGGTGATTAATAAAAATTTAGAAAGCATTAATACTAAAGAGGAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTACCTGCACATAGTAGGTGATTAATAAAAATTTAGAAAGCATTAATACTAAAGAGGAAA  240

Query  241  AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAAATAATATATAAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTAGCCAAAAAATAATATATAAT  300

Query  301  CAGAGAAATAATAGGACTTCTGGaaaaaaaaGATGAGATCAGATTGGTTAGGATCTTTAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGAGAAATAATAGGACTTCTGGAAAAAAAAAGATGAGATCAGATTGGTTAGGATCTTTAC  360

Query  361  TAACATGACAAGAGCATGAAtttttttttCTGTAGATAATAAGTATGAAAGAATTTTAGCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAACATGACAAGAGCATGAATTTTTTTTTCTGTAGATAATAAGTATGAAAGAATTTTAGCT  420

Query  421  TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAAAATTAGCATAATTTGGATCCACATATGCAAATCAATGAATGTAATTCATAATATAA  480
```

```
Query  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCaaaa  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACAGAACTAAACACAAAAACCACGTGATTATCTCAATAGACACAGAAAAGGCCTTCAAAA  540

Query  541  aaaTT  545
            |||||
Sbjct  541  AAATT  545
```

# Sequence 639 matched with Sequence 240

```
Query=   Sequence ID - 639                    nt:     624
Length=624


   SEQ ID NO: 240                  nt:     624

ALIGNMENTS
 Identities = 624/624 (100%), Gaps = 0/624 (0%)

Query  1     GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAAA   60

Query  61    GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAGTGCTC   120

Query  121   TGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATTGTATTAGCA   180

Query  181   AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGCCCACTTCCACTAT   240

Query  241   GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTA   300

Query  301   TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATC   360

Query  361   GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GGCGTAAATCTAACTTTCTTCCCACAACACTTTCTCGGCCTATCCGGAATGCCCCGACGT   420

Query  421   TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TACTCGGACTACCCCGATGCATACACCACATGAAACATCCTATCATCTGTAGGCTCATTC   480
```

```
Query  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTCTCTAACAGCAGTAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAG  540

Query  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CGAAAAGTCCTAATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCC  600

Query  601  CCACCCTACCACACATTCGAAGAA  624
            ||||||||||||||||||||||||
Sbjct  601  CCACCCTACCACACATTCGAAGAA  624
```

# Sequence 641 matched with Sequence 241

```
Query=  Sequence ID 641
Length=421


   SEQ ID NO: 241

ALIGNMENTS
 Identities = 421/421 (100%), Gaps = 0/421 (0%)

Query  1    CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCACGTGCA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCACGTGCA   60

Query  61   GCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATTAAGAAATT   120

Query  121  CGTCATTCGAAACATAGTGGAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGTCATTCGAAACATAGTGGAGGCCGCAGCAGTCAGGGACATTTCTGAAGCGAGCGTCTT   180

Query  181  CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACTGTGTGAGTTGTGCAAT   240

Query  241  TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGCAAGGACCGAACACCCCCACC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGCAAGGACCGAACACCCCCACC   300

Query  301  CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGAGCTGA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCCACCAAAGCCCATGTAAGGAGCTGA   360

Query  361  GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTTCTTAAAGACTGAAGACAGGCTATTCTCTGGAGAAAAATAAAATGGAAATTGTACTTA   420

Query  421  A   421
            |
Sbjct  421  A   421
```

## Sequence 642 matched with Sequence 242

Query=  Sequence ID 642
Length=539


   SEQ ID NO: 242

ALIGNMENTS
 Identities = 539/539 (100%), Gaps = 0/539 (0%)

```
Query  1    TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTCATCTCCCAACCACTGCACTCTTGAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTCATCTCCCAACCACTGCACTCTTGAT  60

Query  61   TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCCTCTCCATT  120

Query  121  TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGCCTCTTTCCTCAC  180

Query  181  TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAGGAAGGTTCTCATTTTT  240

Query  241  GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCCTGGTGGGACACAGGAGTCAT  300

Query  301  GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GACTCCTACCCTCCACCCTCCACACCCACCAGGCATTTAGCAGTCTGTCCTATGCAAGAC  360

Query  361  AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAATTCAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATGAATTCTCAGCCAGGATACCTCAAGGCAGGCAAAGGTGAGTGGAGGGAAAATTCAC  420

Query  421  AAACATTCAGGGTGTGTGGTGCTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAACATTCAGGGTGTGTGGTGCTGGCATCACCATGGCCAAATCCAAGAGGTCTTCCTGGA  480
```

```
Query  481   AGAGGGCCCAAACTGGAACCAAAAGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT   539
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGAGGGCCCAAACTGGAACCAAAAGAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT   539
```

# Sequence 643 matched with Sequence 243

```
Query=   Sequence ID 643
Length=397


   SEQ ID NO: 243

ALIGNMENTS
 Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query  1    CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCACAAA  60

Query  61   AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCCAGAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAATTCCAGAGG  120

Query  121  GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAGAAACCTGAAGTT  180

Query  181  AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGCAAAAAAGGCTAAGCAA  240

Query  241  GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTACAAAGGCAGCACCTAAGCAA  300

Query  301  AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGAGTTGGTGGAAAACGCTAAACTGGC  360

Query  361  AGATTAGATTTTTAAATAAAGATTGGATTATAACTCT    397
            |||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTAGATTTTTAAATAAAGATTGGATTATAACTCT    397
```

## Sequence 644 matched with Sequence 244

Query=  Sequence ID 644
Length=542


   SEQ ID NO: 244

ALIGNMENTS
 Identities = 542/542 (100%), Gaps = 0/542 (0%)

```
Query  1    CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATTTTCT  60

Query  61   GCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCCTCATAGGA  120

Query  121  CCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCTTTGGCCTGAGCG  180

Query  181  GGTTCCATTTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGTTCCATTTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGACAACCTCCAAAAGGTG  240

Query  241  CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTGGTCAAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAAGATTTTCCTTGTGGTCAAGA  300

Query  301  CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTCTGCGAGCCTCGAACACGATGAATCCGCTCGAATGGGCTTGGGCTTTGCCCGGGTGGC  360

Query  361  GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCACGCTCACACGCTGGAAGCACAGCTTTGACGATCTCCACACACGCACAGGCACACACG  420

Query  421  CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCACAGATGATGCCGGCTCATTCTCAGGGGGTGTCTAAGTTCTGCTTTAAATATTTACCC  480
```

```
Query  481   CCTAATTGTACAAACAATAGGGGCATGAGCCTGGTACTCGATAAATGGGGACTTNCTTAA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCTAATTGTACAAACAATAGGGGCATGAGCCTGGTACTCGATAAATGGGGACTTNCTTAA   540

Query  541   AA   542
             ||
Sbjct  541   AA   542
```

## Sequence 645 matched with Sequence 245

```
Query=  Sequence ID - 645                    nt:     649
Length=649


   SEQ ID NO: 245                 nt:     649

ALIGNMENTS
 Identities = 649/649 (100%), Gaps = 0/649 (0%)

Query  1    CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGTCCCC  60

Query  61   GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCGGGGT  120

Query  121  GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAA  180

Query  181  GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTA  240

Query  241  CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCA  300

Query  301  GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCGGGAGCT  360

Query  361  GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCGAGGTGGAGCGCGACAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCGCGTCGAGGTGGAGCGCGACAA  420

Query  421  CCTGGCCGAGGACATCATGCGCGCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCTGGCCGAGGACATCATGCGCGCTCCGGGAGAAATTGCAGGAGGAGATGCTTCAGAGAGA  480
```

```
Query  481  GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGAAGCCGAAAACACCCTGCAATCTTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGAT  540

Query  541  TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCAGGAACAGCATGTCCAAATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTT  600

Query  601  GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCAG  649
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GCGTGACGTACGTANCAATATGAAAGTGTGGCTGCCAAAAACCTTGCAG  649
```

# Sequence 646 matched with Sequence 246

```
Query=   Sequence ID - 646                    nt:     600
Length=600


   SEQ ID NO: 246                  nt:     600

ALIGNMENTS
 Identities = 600/600 (100%), Gaps = 0/600 (0%)

Query  1     GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGGAG  60

Query  61    GCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAG  120

Query  121   TCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTA  180

Query  181   CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGGAC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGGAC  240

Query  241   TGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATGCC  300

Query  301   TGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACATG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACATG  360

Query  361   TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTCTG  420

Query  421   CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTAGG  480
```

```
Query  481  GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTC  540

Query  541  CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CATGTTTGATGTATCTGAGCAGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA  600
```

# Sequence 647 matched with Sequence 247

```
Query=  Sequence ID 647
Length=331


   SEQ ID NO: 247

ALIGNMENTS
 Identities = 331/331 (100%), Gaps = 0/331 (0%)

Query  1    CGAATGTGCAGGTTTGTTACATAGGTATATATATGCCATGATGGAAATATTTAtttttttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAATGTGCAGGTTTGTTACATAGGTATATATATGCCATGATGGAAATATTTATTTTTTTT  60

Query  61   AAGCGTAATTTTGCCAAATAATAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA   120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGCGTAATTTTGCCAAATAATAAAAACAGAAGGAAATTGAGATTAGAGGGAGGTGTTTA   120

Query  121  AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGCAATAAGAATTTA  180

Query  181  GGGAGAAATGTTGTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGGAGAAATGTTGTTCATTATTGGAGGGTAAATGATGTGGTGCCTGAGGTCTGTACGTTA  240

Query  241  CCTCTTAACAATTTCTGTCCTTCAGATGGAAACTCTTTAACTTCTCGTAAAAGTCATATA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCTCTTAACAATTTCTGTCCTTCAGATGGAAACTCTTTAACTTCTCGTAAAAGTCATATA  300

Query  301  CCTATATAATAAAGCTACTGATTTCCAAAAA  331
            |||||||||||||||||||||||||||||||
Sbjct  301  CCTATATAATAAAGCTACTGATTTCCAAAAA  331
```

# Sequence 648 matched with Sequence 248

```
BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.




Query=   Sequence ID 648
Length=41


   SEQ ID NO: 248                                    81.8    3e-22

ALIGNMENTS
 Identities = 41/41 (100%), Gaps = 0/41 (0%)

Query  1    AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  41
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  41
```

## Sequence 649 matched with Sequence 249

```
Query=   Sequence ID - 649                    nt:     425
Length=425


   SEQ ID NO: 249                 nt:     425

ALIGNMENTS
 Identities = 425/425 (100%), Gaps = 0/425 (0%)

Query  1    CaaaaaaaCGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAAAAAACGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGTGAAC  60

Query  61   CACTATATGTGTAATGTAAGTCTTGGAATgagaagagagaaggagaaggaggagagagCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CACTATATGTGTAATGTAAGTCTTGGAATGAGAAGAGAGAAGGAGAAGGAGGAGAGAGCT  120

Query  121  TATTTGTAGAAATAATGGCTGAAAACATCCCAAACTTTCCtttttttGAGGAAAGAAATA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTTGTAGAAATAATGGCTGAAAACATCCCAAACTTTCCTTTTTTTGAGGAAAGAAATA  180

Query  181  GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAATTCTAAAGACACCCCCT  240

Query  241  CTAACATACATTATAATCAAATTGTCAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTAACATACATTATAATCAAATTGTCAAAAGTAAAATACAAAGAGAATCTTTTAAATTGA  300

Query  301  CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTTCAGCAGATTTCTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTCTATAAGAATTTCAGCAGATTTCTC  360

Query  361  AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCaaaaaaaaaa  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGCAGAAACCTTGCAGGCCAACAGGCAGTGGGATGATACATTCAAAGTGCAAAAAAAAAA  420

Query  421  aaaaa  425
            |||||
Sbjct  421  AAAAA  425
```

# Sequence 650 matched with Sequence 250

Query=  Sequence ID 650
Length=633


   SEQ ID NO: 250

ALIGNMENTS
 Identities = 633/633 (100%), Gaps = 0/633 (0%)

```
Query  1    CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACNGCCC   60

Query  61   ATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGATGAAAAGTC   120

Query  121  TTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGACATTTTGAAAGG   180

Query  181  ATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAAGTTCTAAAATCCTTCA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAAGTTCTAAAATCCTTCA   240

Query  241  TTATGAGGGATTCAAAGTATTTATAAAAACACTGCCCTCTAAAAATTTCCTCAGATCTGA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTATGAGGGATTCAAAGTATTTATAAAAACACTGCCCTCTAAAAATTTCCTCAGATCTGA   300

Query  301  AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGTATGGNCTTGGNCCTGAATATACAGTGTTATCCTATGTTTAAAAGGGTGATCCAGACA   360

Query  361  TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCCACTTGGCTATTTCATATCTACCTACA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAGACGCAACTAGTTGGTGCATAAGAAGGCCCCACTTGGCTATTTCATATCTACCTACA   420

Query  421  ATTGACCaaaaaaaaTTTTTTAGGCCAGCAATTATTATTTAGCTTCGCTCTTTCTAGTGC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATTGACCAAAAAAAATTTTTTAGGCCAGCAATTATTATTTAGCTTCGCTCTTTCTAGTGC   480
```

```
Query   481   AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AAGAAACTGCAGGCTGGATCAGTAGTTCAACAGCTAAACAGTCATAAAATAGTCATTGGC   540

Query   541   ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN   600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   ATGTTAAATTTCTTTCAATGCTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGN   600

Query   601   GACNGNATTACTAAACAGGTAAGGATGGGAATA   633
              |||||||||||||||||||||||||||||||||
Sbjct   601   GACNGNATTACTAAACAGGTAAGGATGGGAATA   633
```

# Sequence 651 matched with Sequence 251

```
Query=  Sequence ID - 651                  nt:     251
Length=251


   SEQ ID NO: 251                nt:     251

ALIGNMENTS
 Identities = 251/251 (100%), Gaps = 0/251 (0%)

Query  1     CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTCGAGACCAGTCTGGCCA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTCGAGACCAGTCTGGCCA  60

Query  61    ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGTGGCAAGTG  120

Query  121   CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGAACCTGGGAGGCG  180

Query  181   GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCAAGATT  240

Query  241   CCGTCCATCTC   251
             |||||||||||
Sbjct  241   CCGTCCATCTC   251
```

# Sequence 652 matched with Sequence 252

Query=   Sequence ID 652
Length=593


   SEQ ID NO: 252

ALIGNMENTS
 Identities = 593/593 (100%), Gaps = 0/593 (0%)

```
Query  1    CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAAGTGC  60

Query  61   CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGATACTGCTCT  120

Query  121  TTACAGGATGAGTGGTGTTGTCTTTGGCTgggggggNCTTAAATGTGTTTCTAATGTGTG  180
            ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  121  TTACAGGATGAGTGGTGTTGTCTTTGGCTGGGGGGGNCTTAAATGTGTTTCTAATGTGTG  180

Query  181  TGTCAAATAATTACCTGTTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTCAAATAATTACCTGTTAAACAGACTGCCAATCTGGCTGAAGCCAATGCTTCTGAAGA  240

Query  241  AGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAATACGACCCAATCAATTACAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAATACGACCCAATCAATTACAT  300

Query  301  GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAAGAAACCTCTAGGTCCACCACCTCCATCTTACACGTGTTTCCGTTGTGGTAAACCTGG  360

Query  361  ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACATTATATTAAGAATTGCCCAACAAATGGGGATAAAAACTTTGAATCTGGTCCTAGGAT  420

Query  421  TAAAAAGAGCACTGGAATTCCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAAAAGAGCACTGGAATTCCCAGAAGTTTCATGATGGAAGTGAAAGATCCTAATATGAA  480
```

```
Query   481   AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACTATAGATGCAGAAGCATAT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AGGTGCAATGCTTACCAACACTGGAAAATATGCAATCCAACTATAGATGCAGAAGCATAT   540

Query   541   GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTTCT   593
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   GCAATTGGGAAGAAAGAGAAACCTCCTTNTTACCAGAGAGCCATCTTNTTTCT   593
```

# Sequence 653 matched with Sequence 253

Query=   Sequence ID 653
Length=211


   SEQ ID NO: 253

ALIGNMENTS
 Identities = 211/211 (100%), Gaps = 0/211 (0%)

```
Query  1    GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGTGTTT  60

Query  61   CAATAATTAAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAATAATTAAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCATTGCGCTTT  120

Query  121  GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAGATTATGTGTCAA  180

Query  181  TaaaaaacaaaaattaaaaTCCCAATTTTTA  211
            ||||||||||||||||||||||||||||||
Sbjct  181  TAAAAAACAAAAATTAAAATCCCAATTTTTA  211
```

# Sequence 654 matched with Sequence 254

```
Query=   Sequence ID 654
Length=247


   SEQ ID NO: 254

ALIGNMENTS
 Identities = 247/247 (100%), Gaps = 0/247 (0%)

Query  1    GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGGGGGG  60

Query  61   AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCCTCGGATCAGAGAAAAATGCAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCCTCGGATCAGAGAAAAATGCAG  120

Query  121  ACATGGTGTCACCTGGAtttttttCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATGGTGTCACCTGGATTTTTTTTCTGCCCATGAATGTTGCCAGTCAGTACCTGTCCTCC  180

Query  181  TTGTTTCTCTATTTTTGGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGTTTCTCTATTTTTGGTTATGAATGTTGGGGTTACCACCTGCATTTAGGGGAAAATTG  240

Query  241  TGTTCTG  247
            |||||||
Sbjct  241  TGTTCTG  247
```

# Sequence 655 matched with Sequence 255

Query= Sequence ID 655
Length=244


   SEQ ID NO: 255

ALIGNMENTS
 Identities = 244/244 (100%), Gaps = 0/244 (0%)

```
Query  1    GTCCCCGGGAATCGCGGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTCACA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCCCCGGGAATCGCGGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATTCACA  60

Query  61   AATACTTGGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATACTTGGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGTAAATGCGT  120

Query  121  TTTATGTTTAAATAAAGAGGAAAATTTTTTGaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTATGTTTAAATAAAGAGGAAAATTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  180

Query  181  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT  240

Query  241  TTTT  244
            ||||
Sbjct  241  TTTT  244
```

## Sequence 656 matched with Sequence 256

```
Query=  Sequence ID 656
Length=433


   SEQ ID NO: 256

ALIGNMENTS
 Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query  1    TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCATGCC  60

Query  61   CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTGATCCTTTG  120

Query  121  AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAACTGATTTCCTTAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAACTGATTTCCTTAA  180

Query  181  ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGCCTATTGAAATGATTAG  240

Query  241  GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATGCTGTATACTCACAAAAGTGA  300

Query  301  GATCATTAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GATCATTAATATTGCATGTACTACTTTGAATATCAGGGACCACAGAGAAATAGCATGAGA  360

Query  361  AACGCCTTCCTGCAGTCATGCACTTAAAATGAATATGAACAAAAATGTGGAACTCTGCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AACGCCTTCCTGCAGTCATGCACTTAAAATGAATATGAACAAAAATGTGGAACTCTGCTG  420

Query  421  TCATAGCTCTCCG  433
            |||||||||||||
Sbjct  421  TCATAGCTCTCCG  433
```

# Sequence 657 matched with Sequence 257

Query=  Sequence ID 657
Length=380


   SEQ ID NO: 257

ALIGNMENTS
 Identities = 380/380 (100%), Gaps = 0/380 (0%)

```
Query  1    GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGtttttttCTCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTTCTCT  60

Query  61   TTGAAAGATAGAGATTAATACAACTCTTAAAAAATATAGTCAATAGGTTACTAAGATATT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGAAAGATAGAGATTAATACAACTCTTAAAAAATATAGTCAATAGGTTACTAAGATATT  120

Query  121  GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAATATGAA  180

Query  181  GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACGGAGGT  240

Query  241  TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAGGAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAAAGGAC  300

Query  301  TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGGTGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAATGAAGGTGA  360

Query  361  CTTAAACAGCTTAAAGTTTA    380
            ||||||||||||||||||||
Sbjct  361  CTTAAACAGCTTAAAGTTTA    380
```

# Sequence 658 matched with Sequence 258

Query=  Sequence ID 658
Length=572


   SEQ ID NO: 258

ALIGNMENTS
 Identities = 572/572 (100%), Gaps = 0/572 (0%)

```
Query  1    GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTATAAT  60

Query  61   ATTTGTTTAGTTAATAACAGATAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTGTTTAGTTAATAACAGATAAAAAGGAAAGATTCAAGCCTATTGGATGAGAATTTGT  120

Query  121  ACATTATTTTAGAGCTAATAATAATGGTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATTATTTTAGAGCTAATAATAATGGTTTTCAGTTTAGTGAGGATTTAAAAAATGTTTT  180

Query  181  TGAATCAAACttttttttCTTTATAATCCTTTTTAACTAACTCAGGAAATAAGGTATTATG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAATCAAACTTTTTTTTCTTTATAATCCTTTTTAACTAACTCAGGAAATAAGGTATTATG  240

Query  241  AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACTTCCCACTGTTTGGTCCACTA  300

Query  301  GTGGCTGATTATTTTGTTTGTGGATTATTTGTAATTTTCTTTTTAATTCTTCCTTAAAGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTGGCTGATTATTTTGTTTGTGGATTATTTGTAATTTTCTTTTTAATTCTTCCTTAAAGA  360

Query  361  GCATGGCATTTGGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTTGACC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCATGGCATTTGGAGTCACAGACCTATATTTGAATCCTGTCATTTACTAGCGTTTTGACC  420

Query  421  TTGAACAATTATGCTCAGAGTCTCAGTTTTTTCTTGTAAAGTGATGATGATACTACTTAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTGAACAATTATGCTCAGAGTCTCAGTTTTTTCTTGTAAAGTGATGATGATACTACTTAA  480
```

```
Query   481   CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   CTCACAGGGTTGTAGTGAAGATCAAATGAGATCATGTCTGTANAACACCCTGCCCGGCAC   540

Query   541   TCAATAAGTATTAATAGGAACCCATATACCTC   572
              ||||||||||||||||||||||||||||||||
Sbjct   541   TCAATAAGTATTAATAGGAACCCATATACCTC   572
```

# Sequence 660 matched with Sequence 259

Query=   Sequence ID 660
Length=477


   SEQ ID NO: 259

ALIGNMENTS
 Identities = 477/477 (100%), Gaps = 0/477 (0%)

```
Query  1    TGtttttattttttAAAAGGTATAAACACCaaaaaaaaaaTTAACATTGTATGAAGATGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGTTTTTATTTTTTAAAAGGTATAAACACCAAAAAAAAAATTAACATTGTATGAAGATGG  60

Query  61   AAAATAAGAAGATGCACTTTCTGTAACTTTGTCTAAGGATTTAAATTACTAACTTATGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAATAAGAAGATGCACTTTCTGTAACTTTGTCTAAGGATTTAAATTACTAACTTATGAA  120

Query  121  CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATTATATGGTTTATT  180

Query  181  TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATTTTAGATACTGAAATTG  240

Query  241  AAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAATCTCACCACATATACtttgttana  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAATCTCACCACATATACTTTGTTANA  300

Query  301  tttgtgtattgtagggtgtttgttttgtatttttgtattgtatatgaactttttttAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTGTGTATTGTAGGGTGTTTGTTTTGTATTTTTGTATTGTATATGAACTTTTTTTAAAT  360

Query  361  GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTGACAGTTAAACACATCTTTAAAAGCATAGTCACAGACAAAAGCATACAGTATAAAAAT  420

Query  421  TTCCTTGAAAACTCCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG   477
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTCCTTGAAAACTCCTACAATATTATATTTGGAGGCAGCTTCAGACTGTTTTATTGG   477
```

# Sequence 661 matched with Sequence 260

```
Query=  Sequence ID 661
Length=256


   SEQ ID NO: 260

ALIGNMENTS
 Identities = 256/256 (100%), Gaps = 0/256 (0%)

Query  1    CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGATTTAT  60

Query  61   CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCCCAGTGAGG  120

Query  121  GCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATTATCTCTGTCACA  180

Query  181  GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGTATGGAAAATACCACTT  240

Query  241  GGTTCTACAAATGNGG  256
            ||||||||||||||||
Sbjct  241  GGTTCTACAAATGNGG  256
```

Blast comparison trimmed "NGG" from the 3' end of both sequences and reported 253 identities. The report has been manually corrected for this. "NGG" has been appended to both sequences and identity count has been increased to 256.

## Sequence 663 matched with Sequence 261

```
Query=  Sequence ID - 663              nt:    627
Length=627


   SEQ ID NO: 261              nt:    627

ALIGNMENTS
 Identities = 627/627 (100%), Gaps = 0/627 (0%)

Query  1    GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAGGCAC  60

Query  61   CTGCCACCACGCCTTGCAAATTTTTGTGTTTTTAGTGGAGATGGGGTTTTGCCATGTTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGCCACCACGCCTTGCAAATTTTTGTGTTTTTAGTGGAGATGGGGTTTTGCCATGTTGG  120

Query  121  CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCCAGAGGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGCCTCCCAGAGGGC  180

Query  181  TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTTAATGCCCTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGCATCTTTTAATGCCCTC  240

Query  241  TGAACAAATACATAGAGAAAACTCTCAGAACAATTAAAACCTGCAGAGCAACAGTGTCCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGAACAAATACATAGAGAAAACTCTCAGAACAATTAAAACCTGCAGAGCAACAGTGTCCT  300

Query  301  CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTTCTACTTCTCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCTAATCCATATTTTTCTACTTCTCAG  360

Query  361  ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTTAATGCTAAATATTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATAATTTATGTGTGTGTACTCTTCCTAGACGTACAAGAGACTTTTTAATGCTAAATATTT  420

Query  421  GTCAGTGCTTAACAAAAACTCAATTTCACATTACTCAtattgtttttgtttttaattgaat  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTCAGTGCTTAACAAAAACTCAATTTCACATTACTCATATTGTTTTTGTTTTAATTGAAT  480
```

```
Query  481  gtgaattaaatttttattagttatttgatttggaatgttatgtATGCCATTAACACTATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTGAATTAAATTTTTATTAGTTATTTGATTTGGAATGTTATGTATGCCATTAACACTATT  540

Query  541  AGGGGAATCTCTAGCATTTCTGTATTTTTAAAGAATTTGATTCTTTTGTANATTCTGCCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGGGGAATCTCTAGCATTTCTGTATTTTTAAAGAATTTGATTCTTTTGTANATTCTGCCT  600

Query  601  GTGTGGCATTTTAAACATGTGTGACAT  627
            |||||||||||||||||||||||||||
Sbjct  601  GTGTGGCATTTTAAACATGTGTGACAT  627
```

# Sequence 665 matched with Sequence 262

```
Query=  Sequence ID - 665                    nt:     345
Length=345


   SEQ ID NO: 262                 nt:     345

ALIGNMENTS
 Identities = 345/345 (100%), Gaps = 0/345 (0%)

Query  1    ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGACCCGC  60

Query  61   TATGGGGCCTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATGGGGCCTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACGCCAAGTAC  120

Query  121  ACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGGATCTGGCACTGT  180

Query  181  GGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAATACCACTTCCGCTGTC  240

Query  241  ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAGACCAGTAGACGCTCCTCTAC  300

Query  301  TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA    345
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCTTTGAGACATCACTGGCCTATAATAAATGGGTTAATTTATGTA    345
```

# Sequence 666 matched with Sequence 263

```
Query=  Sequence ID - 666                    nt:     252
Length=252


   SEQ ID NO: 263                nt:     252

ALIGNMENTS
 Identities = 252/252 (100%), Gaps = 0/252 (0%)

Query  1    ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTTGATG  60

Query  61   AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGTTAACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGTTAACA  120

Query  121  GTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAAACTTGTGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAAACTTGTGCT  180

Query  181  TCACCGAAGaaaaatatctaaacatcgaaaaacttaaatattatggaaaaaaaacattgc  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTATGGAAAAAAAACATTGC  240

Query  241  aaaatataaaaT  252
            ||||||||||||
Sbjct  241  AAAATATAAAAT  252
```

# Sequence 669 matched with Sequence 264

Query=  Sequence ID 669
Length=294


   SEQ ID NO: 264

ALIGNMENTS
 Identities = 294/294 (100%), Gaps = 0/294 (0%)

```
Query  1    TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAAGACG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAAGACG  60

Query  61   AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACCCACAGGTC  120

Query  121  CTAAACTACCAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTAAACTACCAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGAGCAGAACCCAAC  180

Query  181  CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGATC  240

Query  241  CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT    294
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAACAGCGCAATCCTATT    294
```

## Sequence 670 matched with Sequence 265

Query=  Sequence ID 670
Length=370


    SEQ ID NO: 265

ALIGNMENTS
 Identities = 370/370 (100%), Gaps = 0/370 (0%)

```
Query  1     GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTACTGGG   60

Query  61    GGCGGACTTggggggggTTGCATACAAAGATAACATATATATCCAACTTTCTGAAATGAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGGACTTGGGGGGGGTTGCATACAAAGATAACATATATATCCAACTTTCTGAAATGAA   120

Query  121   ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGaaaaaaa   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTCACAAGAAAAAAA   180

Query  181   TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTTGTAGATGaaaaaaaTCATTATGT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTTGTAGATGAAAAAAATCATTATGT   240

Query  241   TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAATTTGTATTTAAACAAAAATTT   300

Query  301   AAATTTTGGAATCCTCTAAACATTTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AAATTTTGGAATCCTCTAAACATTTTTGTATCTTTAATTGGTTTATTATTAAATAAATCA   360

Query  361   TATAAAAATT   370
             ||||||||||
Sbjct  361   TATAAAAATT   370
```

# Sequence 671 matched with Sequence 266

```
Query=   Sequence ID 671
Length=353


   SEQ ID NO: 266

ALIGNMENTS
 Identities = 353/353 (100%), Gaps = 0/353 (0%)

Query  1    CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC  60

Query  61   TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT  120

Query  121  TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT  180

Query  181  ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAGAACCATTCTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCAGAACCATTCTAC  240

Query  241  CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA  300

Query  301  TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTA   353
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTA   353
```

# Sequence 672 matched with Sequence 267

```
Query=  Sequence ID 672
Length=433


   SEQ ID NO: 267

ALIGNMENTS
 Identities = 433/433 (100%), Gaps = 0/433 (0%)

Query  1    CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCAGGCC  60

Query  61   TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGCTCTGTCTT  120

Query  121  TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTACCTGAAAGAAACT  180

Query  181  ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCANAACCATTCTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTATTTCANAACCATTCTAC  240

Query  241  CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACAGTACATCCACCCTAACTCTA  300

Query  301  TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAAATGTTGATGGTAATACAGCATTATCTATCACCAATAACCCTTCAGCACTAGATCCCT  360

Query  361  ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCAGTCCAATGGAAATGTTGGATTANAACCAGGCATTGTTTCAATANACTCTCGCTCTG  420

Query  421  TGAACACACATGG  433
            |||||||||||||
Sbjct  421  TGAACACACATGG  433
```

## Sequence 673 matched with Sequence 268

Query= Sequence ID 673
Length=683


   SEQ ID NO: 268

ALIGNMENTS
 Identities = 683/683 (100%), Gaps = 0/683 (0%)

```
Query    1  GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACT   60

Query   61  GCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTTCTTAAGGGCCAAGAAAGC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  GCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTTCTTAAGGGCCAAGAAAGC   120

Query  121  CACNTGNNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCCNTAATNGCTTNN   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACNTGNNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCCNTAATNGCTTNN   180

Query  181  TNTTTGGNNTCNTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTGCNTCCAAAGATANCAT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TNTTTGGNNTCNTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTGCNTCCAAAGATANCAT   240

Query  241  NTNTTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCTTTTCCNCCNGAAAANANNGC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  NTNTTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCTTTTCCNCCNGAAAANANNGC   300

Query  301  CCTTTAAGNGCCNCAAAAAAAAANNGTNTTCTGCANNTTTTCTANTATNACAAANNTTTT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTTTAAGNGCCNCAAAAAAAAANNGTNTTCTGCANNTTTTCTANTATNACAAANNTTTT   360

Query  361  NGTAGAANAAAAATTTTTTTTTAGNGGCTACCCTTTNTTTNTTANNCANNGGAGTTTNTT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  NGTAGAANAAAAATTTTTTTTTAGNGGCTACCCTTTNTTTNTTANNCANNGGAGTTTNTT   420

Query  421  TTTACAAAAAAAAAANATTGGGNCCCCTCCACAACCTTGGGTCTNTAATNGGGGGGTTTT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTACAAAAAAAAAANATTGGGNCCCCTCCACAACCTTGGGTCTNTAATNGGGGGGTTTT   480
```

```
Query  481  TAAATAAANCNTNTNTAAATCCCCCNNNNNNNNNCNNNNNNNNNCCNNNNNNNNNNNNNNN  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAATAAANCNTNTNTAAATCCCCCNNNNNNNNNCNNNNNNNNNCCNNNNNNNNNNNNNNN  540

Query  541  CCCNNNNAAAAAATTTTTNCTCCCCCNCCCTTTTTCTTCCTGCCGGCCCCAATTTAAGCC  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCCNNNNAAAAAATTTTTNCTCCCCCNCCCTTTTTCTTCCTGCCGGCCCCAATTTAAGCC  600

Query  601  CNGGCGCTTGGGGCAAATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGGNT  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CNGGCGCTTGGGGCAAATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGGNT  660

Query  661  TTAAAACCNCGGGGNNNGGGGAA  683
            |||||||||||||||||||||||
Sbjct  661  TTAAAACCNCGGGGNNNGGGGAA  683
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 674 matched with Sequence 269

BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

Query=   Sequence ID 674
Length=49

   SEQ ID NO: 269                                    97.6    8e-27

ALIGNMENTS
 Identities = 49/49 (100%), Gaps = 0/49 (0%)

Query  1    ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG  49
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG  49

## Sequence 675 matched with Sequence 270

```
Query=  Sequence ID - 675                    nt:     591
Length=591


   SEQ ID NO: 270                  nt:     591

ALIGNMENTS
 Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query  1    GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAATACAA  60

Query  61   AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTCAGCTTTGTTTATCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTCAGCTTTGTTTATCC  120

Query  121  TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAAGGATGAAAAGCTTATGCAACATGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAAGGATGAAAAGCTTATGCAACATGC  180

Query  181  TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTATATTTTCATTCTGTAAT  240

Query  241  TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTTAGACCAGAATAAAATTAATT  300

Query  301  ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATATTCTGGTCTTCAAAGGACACACAGAACAGATATCAGCAGAATCACTTAATACTTCAT  360

Query  361  AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGAACAAAAATCACTCAAAACCTGTTTATAACCAAAGAATTCATGAAAAAGAAAGCCTTT  420

Query  421  GCCATTTGTCTTAGAAAGTTATTTTTTaaaaaaaaaTCATACTTACTATTAGTATCTATG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCCATTTGTCTTAGAAAGTTATTTTTTAAAAAAAAAATCATACTTACTATTAGTATCTATG  480
```

```
Query  481  GAAGTATATGTAACAATTTTTATGTAAAGGTCATCTTTCTGTGATAGTGAAAAAATATGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAGTATATGTAACAATTTTTATGTAAAGGTCATCTTTCTGTGATAGTGAAAAAATATGT  540

Query  541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTTTACTAAGTTGAAATGAATACTTTCTGNCTTTGCTAATGGATAGTTATT  591
```

# Sequence 676 matched with Sequence 271

```
Query=   Sequence ID 676
Length=329


    SEQ ID NO: 271

ALIGNMENTS
 Identities = 329/329 (100%), Gaps = 0/329 (0%)

Query  1    CTCAATTCTACTAAAAAGCCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAATTCTACTAAAAAGCCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCTCTGC  60

Query  61   ACAGCAAGTAGCAGTGTCACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAGCAAGTAGCAGTGTCACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCCAGCTCCTC  120

Query  121  CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTCAGACTCAGGCTAAGGGGTCAGGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTCAGACTCAGGCTAAGGGGTCAGGCC  180

Query  181  AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACCCTGCCCCACCTGCCCC  240

Query  241  TTCCCCCTTTGCTGTGACACTTCTTCATCTCAcccccccctgcccccccTCTAGGAGAGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCCCCCTTTGCTGTGACACTTCTTCATCTCACCCCCCCCTGCCCCCCTCTAGGAGAGCT  300

Query  301  GGCTCTGCAGTGGGGGAGGGATGCAGGGA  329
            |||||||||||||||||||||||||||||
Sbjct  301  GGCTCTGCAGTGGGGGAGGGATGCAGGGA  329
```

# Sequence 679 matched with Sequence 272

```
Query=   Sequence ID 679
Length=688


   SEQ ID NO: 272

ALIGNMENTS
 Identities = 688/688 (100%), Gaps = 0/688 (0%)

Query  1     GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACaaa  66
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACAAA  66

Query  67    aaaaaaaaaaaaaaaaaaaaaaaaaanTNTAGACTCGANCAAGCTTATGCANGCNTGCGG  126
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  67    AAAAAAAAAAAAAAAAAAAAAAAAAANTNTAGACTCGANCAAGCTTATGCANGCNTGCGG  126

Query  127   CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC  186
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  127   CCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAGNGAGTCGTATTACAATTC  186

Query  187   ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCAACTTAATCG  246
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  187   ACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCAACTTAATCG  246

Query  247   CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACCGATCG  306
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  247   CCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATANCGAANAGGCCCGCACCGATCG  306

Query  307   CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG  366
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  307   CCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAANGGAAATTGTAAGCGTTAATATTTTG  366

Query  367   TTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC  426
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  367   TTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATC  426

Query  427   GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT  486
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  427   GGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTT  486
```

```
Query  487   TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC   546
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  487   TGGAACAANAGTCCACTNTTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTC   546

Query  547   TATCAGGGCGATGGCCCACTACGTGAACCATCNCCCTAATCAAGTTTTTTGGGGTCGAGG   606
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  547   TATCAGGGCGATGGCCCACTACGTGAACCATCNCCCTAATCAAGTTTTTTGGGGTCGAGG   606

Query  607   NGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCTTGACGGGGA   666
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  607   NGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCTTGACGGGGA   666

Query  667   AAGCCCGGCGAACGTGGCGAAA    688
             ||||||||||||||||||||||
Sbjct  667   AAGCCCGGCGAACGTGGCGAAA    688
```

Blast comparison trimmed "GNANCN" from the 5' end of both sequences and reported 682 identities. The report has been manually corrected for this. "GNANCN" has been prepended to both sequences and identity count has been increased to 688.

# Sequence 682 matched with Sequence 273

```
Query=   Sequence ID 682
Length=271


   SEQ ID NO: 273

ALIGNMENTS
 Identities = 271/271 (100%), Gaps = 0/271 (0%)

Query  1     CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTGGCTG   60

Query  61    GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTCTCAACTAC   120

Query  121   TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTGATGGAAAAGATG   180

Query  181   CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAACTGAAACTTTGCTTAACNA   240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAACTGAAACTTTGCTTAACNA   240

Query  241   CCGAATGGNGGGGANCTTTTCCAACGNTTTT   271
             |||||||||||||||||||||||||||||||
Sbjct  241   CCGAATGGNGGGGANCTTTTCCAACGNTTTT   271
```

## Sequence 683 matched with Sequence 274

Query=   Sequence ID 683
Length=213


    SEQ ID NO: 274

ALIGNMENTS
 Identities = 213/213 (100%), Gaps = 0/213 (0%)

```
Query  1    TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTAATCC  60

Query  61   CTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAAGGCTGTGC  120

Query  121  CTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACTGGTGGCTTTATA  180

Query  181  AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC  213
            |||||||||||||||||||||||||||||||||
Sbjct  181  AGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC  213
```

# Sequence 684 matched with Sequence 275

```
Query=  Sequence ID - 684                    nt:     545
Length=545


   SEQ ID NO: 275                  nt:     545


ALIGNMENTS
 Identities = 545/545 (100%), Gaps = 0/545 (0%)

Query  1    GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGATGCC  60

Query  61   CANGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAACTATTGGA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CANGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAACTATTGGA  120

Query  121  TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAAGCAGATGCAGCA  180

Query  181  GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCAAGAACACCATGATGCG  240

Query  241  CAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTGGAGAAACTGCTGCCTCATAT  300

Query  301  CCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGANATCAGGGACATGTT  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGACCTCACTGANATCAGGGACATGTT  360

Query  361  GCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCTGGCCAATAAGGTGCCAGCTGCTGCCCGTGCTGGTGCCATTGCCCCATGTGAAGTCAC  420

Query  421  TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTTCCAGGCTTTAGG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTGCCAGCCCAGAACACTGGTCTCGGGCCCGATAAGACCTCCTTTTTCCAGGCTTTAGG  480
```

```
Query  481  TATCACCACTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATCACCACTAAAATCTCCAGGGGCACCATTGAAATCCTGAGTGATGTGCACTGATCAAG  540

Query  541  ACTGG  545
            |||||
Sbjct  541  ACTGG  545
```

# Sequence 685 matched with Sequence 276

Query=  Sequence ID 685
Length=260


   SEQ ID NO: 276

ALIGNMENTS
 Identities = 260/260 (100%), Gaps = 0/260 (0%)

```
Query  1    GGAAAGGGCCATTTTATTGCCTAAAACCACCTGGNTTTTNAGGTAACAGTTCCAACATGT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAAGGGCCATTTTATTGCCTAAAACCACCTGGNTTTTNAGGTAACAGTTCCAACATGT  60

Query  61   CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAGTACTTGAT  120

Query  121  AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTGTCAGGGAGCCAT  180

Query  181  GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAGCAGAACATGGGATCAC  240

Query  241  AAGGTGGAACCNTTCCNTTT  260
            ||||||||||||||||||||
Sbjct  241  AAGGTGGAACCNTTCCNTTT  260
```

# Sequence 686 matched with Sequence 277

Query=   Sequence ID 686
Length=603


   SEQ ID NO: 277

ALIGNMENTS
 Identities = 603/603 (100%), Gaps = 0/603 (0%)

```
Query    1  GACCCCTTCCTTACACCTTATACAAAAAAACTGAAACTGGACCCCTTCCTTACACCTTAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACCCCTTCCTTACACCTTATACAAAAAAACTGAAACTGGACCCCTTCCTTACACCTTAT   60

Query   61  ACAAAAATTAACTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAATTAAGATGG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  ACAAAAATTAACTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAATTAAGATGG   120

Query  121  ATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAAAACCTAGGCCAT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAAAACCTAGGCCAT   180

Query  181  ACCATTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAACACCAAAAGCAATGGCA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCATTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAACACCAAAAGCAATGGCA   240

Query  241  ACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAAGAGCTTCAGCACAGCAGAAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAAGAGCTTCAGCACAGCAGAAG   300

Query  301  AGACTATCGTCAGAGTGAACAGGCAACCCACAGAATGGAAGAAAATTCTTGCAATCTATC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGACTATCGTCAGAGTGAACAGGCAACCCACAGAATGGAAGAAAATTCTTGCAATCTATC   360

Query  361  CATCTGACAAGGGGCTAATATCCAAAATCTACAAAGAACTTAAACAAATTTACAAGGAAA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CATCTGACAAGGGGCTAATATCCAAAATCTACAAAGAACTTAAACAAATTTACAAGGAAA   420

Query  421  AACACAAACAACCCCATCAAAAAGTGGGCTAAGGATGTGAACAGACACTTCTCAAAAGAA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AACACAAACAACCCCATCAAAAAGTGGGCTAAGGATGTGAACAGACACTTCTCAAAAGAA   480
```

```
Query  481  AACATTTATGCAGCCAACAAACATGAAAAAAAGTTCATCATCACTGCTCATTAGAGACAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACATTTATGCAGCCAACAAACATGAAAAAAAGTTCATCATCACTGCTCATTAGAGACAT  540

Query  541  GCAAATCAAAACCACAATGAGATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCAAATCAAAACCACAATGAGATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAA  600

Query  601  TGT  603
            |||
Sbjct  601  TGT  603
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 687 matched with Sequence 278

```
Query=  Sequence ID - 687              nt:     268
Length=268


   SEQ ID NO: 278              nt:     268

ALIGNMENTS
 Identities = 268/268 (100%), Gaps = 0/268 (0%)

Query  1    TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCCCCTG  60

Query  61   CCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGTCATTTTGT  120

Query  121  TGACATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGACATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAACCAAAGGCCACCC  180

Query  181  TGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTaaaaaaaaaaaaaaa  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTGTAAAAAAAAAAAAAAA  240

Query  241  aaaaaaaaaaaaaaaaaaaaaaaaaaaa  268
            ||||||||||||||||||||||||||||
Sbjct  241  AAAAAAAAAAAAAAAAAAAAAAAAAAAA  268
```

## Sequence 688 matched with Sequence 279

```
Query=   Sequence ID - 688                    nt:     569
Length=569


   SEQ ID NO: 279                 nt:     569

ALIGNMENTS
 Identities = 569/569 (100%), Gaps = 0/569 (0%)

Query  1     CTTTAGCCAGCCTGATCAGaaaaaaaaCAAAAGAAGAGGAAAGACGTAGATTACCAACATC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTTAGCCAGCCTGATCAGAAAAAAACAAAAGAAGAGGAAAGACGTAGATTACCAACATC  60

Query  61    AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTAAAAGCATAATTAGAGAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTAAAAGCATAATTAGAGAA  120

Query  121   TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGACAAATTTCTTGAA  180

Query  181   AGATAAATTATGAAATTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGATAAATTATGAAATTTCATTCTGAAAGAACTACATGACCTTAATTGTCTTACATCTAT  240

Query  241   TAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAAGAAAACTCTAGGCCCAGATG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAAGAAAACTCTAGGCCCAGATG  300

Query  301   GCATCAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCATCAAAATAATATTCAGATGAATGAAATGGAGAAAGGATAGCCTTTTCAACAAATGGT  360

Query  361   GGTGGAACAATTGGATTTCCATATGCaaaaaaaTAGAGATGGACGCAGAGGTGTGTGCTT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GGTGGAACAATTGGATTTCCATATGCAAAAAAATAGAGATGGACGCAGAGGTGTGTGCTT  420

Query  421   AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCCATT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AGGAGGCTGAGGTGAGAGGATTGTTTGAGGCCAGCCTGGGCAACATAGCAAGACCCCATT  480
```

```
Query  481  TCAAAAACAAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCAAAAACAAAAATAAAGAACTTGTAGCCTTACCTTGTGCCATATTATGAAAATGTATCA  540

Query  541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
            |||||||||||||||||||||||||||||
Sbjct  541  TAGGCTTAAATGTGAAACGTAAAACAAAA  569
```

# Sequence 689 matched with Sequence 280

```
Query=   Sequence ID 689
Length=492


   SEQ ID NO: 280


ALIGNMENTS
 Identities = 492/492 (100%), Gaps = 0/492 (0%)

Query  1    CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttttttt  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTT  60

Query  61   CTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTACTAAG  120

Query  121  ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGAAAAT  180

Query  181  ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACATGACG  240

Query  241  GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAGAGAA  300

Query  301  AGGACTACAGAGCCCCGAATTAATACTAATAGAAGGGCAATGCTTTTAGATTAAAATGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGGACTACAGAGCCCCGAATTAATACTAATAGAAGGGCAATGCTTTTAGATTAAAATGAA  360

Query  361  GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTTGAAG  420

Query  421  GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATGACGC  480
```

```
Query  481  AGGGAGAATTGC  492
            ||||||||||||
Sbjct  481  AGGGAGAATTGC  492
```

# Sequence 690 matched with Sequence 281

```
Query=   Sequence ID 690
Length=355


   SEQ ID NO: 281

ALIGNMENTS
 Identities = 355/355 (100%), Gaps = 0/355 (0%)

Query  1    CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAAAACA  60

Query  61   ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGaaaaaaaGCCTTTTA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGAAAAAAAGCCTTTTA  120

Query  121  AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTCTAACTGAAGTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTCTAACTGAAGTGA  180

Query  181  GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCTTCTCCTAGTGTTCTTC  240

Query  241  CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAAAGCCTCCTAGTCACTGGATGGGAAGCACTGTTGAAAATTCCAACCAAAACAGGGAGC  300

Query  301  TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACTTAGATTTCAGATTT   355
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTCAAACTTAGATTTCAGATTT   355
```

## Sequence 691 matched with Sequence 282

Query=   Sequence ID 691
Length=619


   SEQ ID NO: 282

ALIGNMENTS
 Identities = 619/619 (100%), Gaps = 0/619 (0%)

```
Query  1    CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTCAGCT  60

Query  61   ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGTAGTGAGCC  120

Query  121  AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCaaaaagaaa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  121  AGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGTCTCAAAAAGAAA  180

Query  181  aaaaaaaTTGCTAATTTTAACAAATCACAAAACTGACTCAGGCAAGTTGTCTGACTCAA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAAAAATTGCTAATTTTAACAAATCACAAAACTGACTCAGGCAAGTTGTCTGACTCAA  240

Query  241  AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACTGGTCATTTACGTAAAATAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACTGGTCATTTACGTAAAATAGT  300

Query  301  GTTCATTAAATTTTTGGTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTTCATTAAATTTTTGGTTCATTTAGGATAATCATTTTAAATGAGACTGTATTTGAGACT  360

Query  361  GtatacacatacatatacatgtttacacacatatacgtacaatatatgtacatTCTATCT  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTATACACATACATATACATGTTTACACACATATACGTACAATATATGTACATTCTATCT  420

Query  421  AAAAGATCATACATGTGTGTACATATATGTTTTTAAAAGTCAAACTGACATATTAATGGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAAGATCATACATGTGTGTACATATATGTTTTTAAAAGTCAAACTGACATATTAATGGA  480
```

```
Query  481  AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACAGTGCTTACATCTCTGGTAGTGATTTTCTATTAGCAGCAGCCCTACATATGCTGCGT  540

Query  541  CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTCTGAACAGCATGTCAGTGCCATGACTGTCTAAACATGCAAATATGACTGACAGACTCT  600

Query  601  TGAGACAGCTTTCACCTTG  619
            |||||||||||||||||||
Sbjct  601  TGAGACAGCTTTCACCTTG  619
```

# Sequence 692 matched with Sequence 283

```
Query=   Sequence ID 692
Length=328


   SEQ ID NO: 283

ALIGNMENTS
 Identities = 328/328 (100%), Gaps = 0/328 (0%)

Query  1    AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATGCAGA  60

Query  61   CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGTGCCACCTT  120

Query  121  CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAACTGCTCTGGCACTTCTGTCAAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAACTGCTCTGGCACTTCTGTCAAGC  180

Query  181  CTCCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTTGCAAAGACTCAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAGATTTGCAAAGACTCAC  240

Query  241  GTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGAAACTAAGAAGCTTAATGAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGAAACTAAGAAGCTTAATGAAA  300

Query  301  AGAAATAAAATGCCTATGTTGTTGTTCT  328
            ||||||||||||||||||||||||||||
Sbjct  301  AGAAATAAAATGCCTATGTTGTTGTTCT  328
```

# Sequence 693 matched with Sequence 284

Query=  Sequence ID 693
Length=563


   SEQ ID NO: 284

ALIGNMENTS
 Identities = 563/563 (100%), Gaps = 0/563 (0%)

```
Query  1    CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCTTTCA  60

Query  61   TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAACACGCTAGG  120

Query  121  TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTCATTCTATAACTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTCATTCTATAACTA  180

Query  181  AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCATGCTAAAAATCACTGG  240

Query  241  ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATggggggggTCATACTTGTAATCCC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATGGGGGGGGTCATACTTGTAATCCC  300

Query  301  AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCACTTTGGGAGGCCGAGGTGGGAAAATTGCTTGAGGCCAGGAGTTCGAAACCAGCCTG  360

Query  361  GGCAACACAGTGAGACCCCATCTCCACaaaaaaaaaaaattaaaaaacaaaacaaaaCAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGCAACACAGTGAGACCCCATCTCCACAAAAAAAAAAAATTAAAAAACAAAACAAAACAT  420

Query  421  TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAGCTGGGCATGGTGGTACACGCCTGTAGTCCCAGCTACTCAGGAGCCTGAAGTGAGAGG  480
```

```
Query  481   ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATCACTGAAGCCCAGGAGGTAGAGCTATGACTGTAGTGAGCTATGACTGTGCCACTACAC   540

Query  541   TCCACCTGGGTGACAGGGGACTC   563
             |||||||||||||||||||||||
Sbjct  541   TCCACCTGGGTGACAGGGGACTC   563
```

# Sequence 694 matched with Sequence 285

```
Query=   Sequence ID 694
Length=257


   SEQ ID NO: 285

ALIGNMENTS
 Identities = 257/257 (100%), Gaps = 0/257 (0%)

Query  1    CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGCTATT  60

Query  61   CCTAGGCCTGAGTTTTATTTTGTTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTAGGCCTGAGTTTTATTTTGTTGACACAGAAATAAATTANAAGGCCAAGCGTGGTGGC  120

Query  121  ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAGGAGTTCAAGGC  180

Query  181  TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGACAGACTAAGACGCTGTC  240

Query  241  TCaaaaaaaaacaaaaa  257
            |||||||||||||||||
Sbjct  241  TCAAAAAAAAACAAAAA  257
```

# Sequence 696 matched with Sequence 286

Query=  Sequence ID 696
Length=602


   SEQ ID NO: 286

ALIGNMENTS
 Identities = 602/602 (100%), Gaps = 0/602 (0%)

```
Query   1    GGTTATCAATGAGATTAAGAGACAACTAGAGTaaaaacaaaagaaaagaaaagaaangaa  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGTTATCAATGAGATTAAGAGACAACTAGAGTAAAAACAAAAGAAAAGAAAAGAAANGAA  60

Query   61   aaCAACAGAAGCTCTATTAACTGACCTCTAACCAATACAACAGGTTAACTGATGTTCTCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AACAACAGAAGCTCTATTAACTGACCTCTAACCAATACAACAGGTTAACTGATGTTCTCC  120

Query   121  ATTCTGTATATAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATTCTGTATATAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGGCTTGTAGGACAC  180

Query   181  TTTCTAGTTCATCTGAGCACTTTTGTTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TTTCTAGTTCATCTGAGCACTTTTGTTCTCAGCAGTTGAGCTGTATACTTAGCAACATTT  240

Query   241  GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATTGAAATACATAATTTAATTAA  300

Query   301  ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATATTATATAAAGGAATGGAATACGAGTTGGACAAGAAAAAGAGTTAAATCTGAAGGTTA  360

Query   361  GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GGTAAAAAGAGCAACTTCTTTTCTCTGTTTTGCAGGTTGGCAAAATCATTTAAAAACAAT  420

Query   421  TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAAACTAGGCATCAAAGA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TGGAAGTATTATATGTTCTGCATTAAGTTGTCATTTTACTTAAAAACTAGGCATCAAAGA  480
```

```
Query  481  TGATGCATAATAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TGATGCATAATAAATTTAGTGTATGCAAGAATGACTGCTTGGGACCTCAATATATGAATT  540

Query  541  CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTTAATCCAAGGAAAGTCCTTGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCA  600

Query  601  TT  602
            ||
Sbjct  601  TT  602
```

# Sequence 697 matched with Sequence 287

```
Query=   Sequence ID 697
Length=306


   SEQ ID NO: 287

ALIGNMENTS
 Identities = 306/306 (100%), Gaps = 0/306 (0%)

Query  1    GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCCCAGC  60

Query  61   ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATCCTGGCTAA  120

Query  121  CACAGTGAAACCCTGTCTCTACTTaaaaaataaaaaaaTTAGCCAGGCGTGGTGGTGGGC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACAGTGAAACCCTGTCTCTACTTAAAAAATAAAAAAATTAGCCAGGCGTGGTGGTGGGC  180

Query  181  GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCG  240

Query  241  GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGCTTGCANTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGAGCGACAGAGCGAGACT  300

Query  301  CTGTCT  306
            ||||||
Sbjct  301  CTGTCT  306
```

## Sequence 698 matched with Sequence 288

Query=   Sequence ID 698
Length=419


   SEQ ID NO: 288

ALIGNMENTS
 Identities = 419/419 (100%), Gaps = 0/419 (0%)

```
Query  1    TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTTCTTTATCTTTGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCATTAGAATCCAAGCTTTGAAAATTTCTGATTAATGCTCATGTATTTCTTTATCTTTGT  60

Query  61   TTTTCCTTGTGAAGAAAGACTTTCACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTCCTTGTGAAGAAAGACTTTCACCACTGTCTGAGTGATGATGCTGTTGATAAGGATG  120

Query  121  ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATGTCGATGACTACTATATTGCATCTCTCAGGAACAGCTGATGGGAAGGGAGGGGCTGCT  180

Query  181  GAGTTCCCTTGTTCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAGTTCCCTTGTTCTAGCTAGCAGCACGCTCCTCANAGAGGGGGCCGAGTTACAGACAGC  240

Query  241  AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGCCGCATTCTCATGCAAAATTAGTTTTAAACTGCTAGTGTGGGCATCGGTACCTTTTGC  300

Query  301  CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTGGGTGATACCGAAGAATTGTTGAGGATTTAGTATGCTCCGTAGAGACAGTTCAGCCAG  360

Query  361  TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT  419
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCATTTCTGCATTGGAGAGACTTCTCATACTTTCTTTGAAGACTCATAGAAAGCTGGAT  419
```

# Sequence 699 matched with Sequence 289

Query=   Sequence ID 699
Length=626


   SEQ ID NO: 289

ALIGNMENTS
 Identities = 626/626 (100%), Gaps = 0/626 (0%)

```
Query  1    ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGaaaaaanTGNCTTCCTTACCTAT  60
            ||||||||||||||||||||||||||||||||||||| |||||| |||||||||||||||
Sbjct  1    ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGAAAAAANTGNCTTCCTTACCTAT  60

Query  61   TGCCTCTGATNTTTACTTGCTTAAAtttttttttATTGNAAATCCAGAAAAAGNGGATTTA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGCCTCTGATNTTTACTTGCTTAAATTTTTTTTTATTGNAAATCCAGAAAAAGNGGATTTA  120

Query  121  GAGAACAACACTAACTCCCACCTAATCTATGACAganatgtacaananagtacctgtgaa  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGAACAACACTAACTCCCACCTAATCTATGACAGANATGTACAANANAGTACCTGTGAA  180

Query  181  aaatgtgaaagnatntgaaaaatgtAACCTTTGGCAGCCTGAGCATAGTCAACCAGAAAA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAATGTGAAAGNATNTGAAAAATGTAACCTTTGGCAGCCTGAGCATAGTCAACCAGAAAA  240

Query  241  ACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAt  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTTATTTGGTCCATAAGGATTAT  300

Query  301  tttttcaacttttttttCAAGTGTATTATTATGTCATTTCCCACGTAGGTTACTGATACC  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTTCAACTTTTTTTTCAAGTGTATTATTATGTCATTTCCCACGTAGGTTACTGATACC  360

Query  361  TGAAGACTTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAAGACTTTTTNCACCTTTAACCTTNCTCGTTGAGGAGCTTTGTANTCTAATAAAAGAG  420

Query  421  AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAATATAAGTAAATGTTAGATATATGGGNGGATAATGGTAACTATGTGCTTAAAGAGGTA  480
```

```
Query  481  TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TAAAAGAAGGGTAGGGAGCAGATAAGACAAAGGAAGGGCTATATTATAANGAAGAATATT  540

Query  541  CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCAAGTAGGGAAGAGAAAAAGATATGTTATCCATATAATATTTTATGTGCAGTAGAGAAC  600

Query  601  ATGTTCTATAGAANAGACAGAAGATG  626
            ||||||||||||||||||||||||||
Sbjct  601  ATGTTCTATAGAANAGACAGAAGATG  626
```

# Sequence 700 matched with Sequence 290

```
Query=   Sequence ID 700
Length=623


   SEQ ID NO: 290

ALIGNMENTS
 Identities = 623/623 (100%), Gaps = 0/623 (0%)

Query  1    CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAGATAC  60

Query  61   AAAAATTAGCCAGATGTGGTGGTGCGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAATTAGCCAGATGTGGTGGTGCGTGCCTGTAGTTCCAGATACTGGAAAGACTGAGGC  120

Query  121  AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGAGGATTGCTTGAGCATGGGAAGTTGAGGCTGCAATGAGCTGTGATTACGCCACTACA  180

Query  181  CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCaaaaaaaaaattgaattcagctaaaa  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCAAAAAAAAAAATTGAATTCAGCTAAAA  240

Query  241  ataataaaattttaaaataattttaaaaaGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATAATAAAATTTTAAAATAATTTTAAAAAGCCCTCAACAGCTTTGTTTTTCTCTCCTTGC  300

Query  301  CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTGCTGCGAGCCAGGACAAGCGGTGGG  360

Query  361  AAATGCAATCACAGCGTGAAATCTCTGTGTTCAGAGACACGCAGGAAGCAGGTGAACCAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAATGCAATCACAGCGTGAAATCTCTGTGTTCAGAGACACGCAGGAAGCAGGTGAACCAT  420

Query  421  GAAGGGCCAACACATGCCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAGGGCCAACACATGCCCCCAGTTAGCAGGGTGTAGAGACCGGGGCAGGGCTTTCTTCT  480
```

```
Query  481  TCCTTCTGGGTTATAAATATCCATGTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCCTTCTGGGTTATAAATATCCATGTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGA  540

Query  541  TGCTGGACAGGCGCTCGCACTTTCTGGGCAGGGCANGGGGCTCAAAGGCAGGACAGCTGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCTGGACAGGCGCTCGCACTTTCTGGGCAGGGCANGGGGCTCAAAGGCAGGACAGCTGG  600

Query  601  GCAAAAGCACCTTGCGTGGGCCC  623
            |||||||||||||||||||||||
Sbjct  601  GCAAAAGCACCTTGCGTGGGCCC  623
```

## Sequence 701 matched with Sequence 291

```
Query=   Sequence ID - 701                    nt:     579
Length=579


   SEQ ID NO: 291                  nt:     579

ALIGNMENTS
 Identities = 579/579 (100%), Gaps = 0/579 (0%)

Query  1    CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGCTCGT  60

Query  61   GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTACATCAACTC  120

Query  121  TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGCTCGGGAGCAGTAATGAATGCAATGGAAACAAACCTCGTTGGAAGTGACAAATATGC  180

Query  181  TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACAATGATGGCTTTGAAGG  240

Query  241  TAATTAAAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAAATGGTTTATGGAAGAAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAATTAAAATTATCAAATTGGTGCTTGATTTCTGCTTTTAAAATGGTTTATGGAAGAAAA  300

Query  301  TATGATTAAAGTTTTGTATTGTTTTCCTTCCTATAGAAGATGGAGCCAGAATGGCATGCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATGATTAAAGTTTTGTATTGTTTTCCTTCCTATAGAAGATGGAGCCAGAATGGCATGCT  360

Query  361  AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAGTTTTTTCTTTTCTTTAGTGTTATATATGACTTCTCCTCAATTGTCACCCATTGATCT  420

Query  421  TTACCACTGTTAATAATGGATGATATTCAAAATACCTTATTTCAGTGATTCTAAGGCACC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTACCACTGTTAATAATGGATGATATTCAAAATACCTTATTTCAGTGATTCTAAGGCACC  480
```

```
Query  481  ATTGATTAGAAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTGATTAGAAACTGCATTATTATTTATGTGTCCCTAAAAGCTACCTATTAAGCTGTTAC  540

Query  541  ACCCACCATTTTTCTGTTAAGAAAATCCTGATTTCAGAA  579
            |||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACCCACCATTTTTCTGTTAAGAAAATCCTGATTTCAGAA  579
```

# Sequence 702 matched with Sequence 292

Query= Sequence ID 702
Length=709


   SEQ ID NO: 292


ALIGNMENTS
 Identities = 709/709 (100%), Gaps = 0/709 (0%)

```
Query  1    GTNNTCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA   64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTNNTCCTCTCGGAACGCGCCTTNTGTAGCCAGGTGCTACCAGACCNAATACACGGTTGTTCCA   64

Query  65   GCTTGCGCATTCACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAT   124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65   GCTTGCGCATTCACCGATGGCGTAGATATCCGGATCGGAAGTCTGGCAGGAATCATTAAT   124

Query  125  GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG   184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125  GACAATACCCCCACGCGGAGCAACGTCCAGACCACACTGGGTTGCCAGCTTATCGCGCGG   184

Query  185  ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG   244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  185  ACGGATACCGGTAGAGAAGACGATAAAGTCGACTTCCAGTTCGCTGCCGTCGGCAAAACG   244

Query  245  CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG   304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  CATGGTTTTACGCGCTTCAACACCTTCCTGCACAATCTCAAGGGTGTTTTTGCTGGTGTG   304

Query  305  AACGCGCACGCCCATACTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG   364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  AACGCGCACGCCCATACTTTCGATTTTGCGACGCAGCTGCTCGCCGCCCATCTGATCAAG   364

Query  365  CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT   424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365  CTGTTCTGCCATCAGCATAGGGGCAAATTCGATAACGTGGGTTTCAATACCTAAGTTTTT   424

Query  425  CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA   484
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  425  CAGCGCGCCTGCGGCTTCCAGACCTAACAGGCCGCAATTCGAGCTCGGCCGACTTGGCCA   484
```

```
Query  485  ATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACT  544
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  485  ATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACT  544

Query  545  GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT  604
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545  GGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCT  604

Query  605  GGCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTCCAACAGTTGCGCACCTGAAT  664
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  605  GGCGTAATAGCGAAAGAGGCCCGCACCCGATCGCCCTTTCCAACAGTTGCGCACCTGAAT  664

Query  665  GGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT  709
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  665  GGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT  709
```

Blast comparison trimmed "GTNN" from the 5' end of both sequences and reported 705 identities. The report has been manually corrected for this. "GTNN" has been prepended to both sequences and identity count has been increased to 709.

# Sequence 703 matched with Sequence 293

```
Query=  Sequence ID 703
Length=471


   SEQ ID NO: 293

ALIGNMENTS
 Identities = 471/471 (100%), Gaps = 0/471 (0%)

Query  1    CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCA  60

Query  61   TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGA  120

Query  121  CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAG  180

Query  181  CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGC  240

Query  241  CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAG  300

Query  301  TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCT  360

Query  361  GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTG  420

Query  421  AAGGAAGAAGTGGGGTGGAAGAAGTGGGGGTGGGACGACAGTGAAATCTAA    471
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGGAAGAAGTGGGGTGGAAGAAGTGGGGGTGGGACGACAGTGAAATCTAA    471
```

# Sequence 704 matched with Sequence 294

```
Query=   Sequence ID 704
Length=495


   SEQ ID NO: 294

ALIGNMENTS
 Identities = 495/495 (100%), Gaps = 0/495 (0%)

Query  1    CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTTGTATGATGCCAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGTATTCAAGAACTACTGTAATGCATTAGTGGTCTGGCTTCATTTTGTATGATGCCAG  60

Query  61   ATCCTTAATTTACCCAGCACAATCATTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCTTAATTTACCCAGCACAATCATTTCAGTAGTTTCCTATGGCTCCTGCAAAAATGCA  120

Query  121  AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAGGTAGTAGTCGCT  180

Query  181  AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAACTAGAACTTCTGTAGAAACAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAACTAGAACTTCTGTAGAAACAC  240

Query  241  ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAACTGACATAATTGTGATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTAAAACTGACATAATTGTGATT  300

Query  301  TATTAACATGAATTAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAAATAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATTAACATGAATTAAAATGCCCAACCAGTGCTTCAGTGTGACAGTATATTTAAAATAAA  360

Query  361  AAAGAAATTAAAGGTCATATACTGTACTACTTTCACAAAGATCCACAGTTTTGCAAAAGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAAGAAATTAAAGGTCATATACTGTACTACTTTCACAAAGATCCACAGTTTTGCAAAAGA  420

Query  421  CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTGTCATATGTACAATGCTATATATCAAATGAGAAAAGCTGTAAGCAATTATATACGCA  480
```

```
Query  481  AAAGAAATGGCAGTA  495
            |||||||||||||||
Sbjct  481  AAAGAAATGGCAGTA  495
```

## Sequence 705 matched with Sequence 295

Query=   Sequence ID 705
Length=531


   SEQ ID NO: 295

ALIGNMENTS
 Identities = 531/531 (100%), Gaps = 0/531 (0%)

```
Query  1    TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTCCAGTCCTTTCATTTAGTATAAAAGAAATACTGAACAAGCCAGTGGGATGGAATTGAA   60

Query  61   AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAACTAATCATGAGGACTCTGTCCTGACACAGGTCCTCAAAGCTAGCAGAGATACGCAG   120

Query  121  ACATTGTGGCATCTGGGTAGAAGAATACTGTATtgtgtgtgcagtgcacagtgtgtggtg   180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATTGTGGCATCTGGGTAGAAGAATACTGTATTGTGTGTGCGCAGTGCACAGTGTGTGGTG   180

Query  181  tgtgCACACTCATTCCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG   240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTGCACACTCATTCCTTCTGCTCTTGGGCACAGGCAGTGGGTGTAGAGGTAACCAGTAG   240

Query  241  CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTAAGGAATCACAAAGGTAAACT   300

Query  301  ACCCAACCACATGCCACGTAATATTTCAGCCATTCAGAGGAAACTGTTTTCTCTTTATTT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACCCAACCACATGCCACGTAATATTTCAGCCATTCAGAGGAAACTGTTTTCTCTTTATTT   360

Query  361  GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCTTATATGTTAATATGGTTTTTAAATTGGTAACTTTTATATAGTATGGTAACAGTATGT   420

Query  421  TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAATACACACATACATATGCACACATGCTTTGGGTCCTTCCATAATACTTTTATATTTGT   480
```

```
Query  481  AAATCAATGTTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTTGTAAA  531
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAATCAATGTTTTTGGAGCAATCCCAAGTTTAAGGGAAATATTTTTGTAAA  531
```

## Sequence 706 matched with Sequence 296

```
Query=   Sequence ID - 706                    nt:     496
Length=496


   SEQ ID NO: 296                  nt:     496


ALIGNMENTS
 Identities = 496/496 (100%), Gaps = 0/496 (0%)

Query  1    CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAACCCTCTCTCCTCAGCGCTTCTTCTTTCTTGGTTTGATCCTGACTGCTGTCATGGCGT  60

Query  61   GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTCGGGCAAAG  120

Query  121  AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGACCCGGGAGCTGC  180

Query  181  CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAGCTGATGAGCAACTTGG  240

Query  241  ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTGTGTCTTCCTGTCCTGCATCG  300

Query  301  CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAGATAAGCAGCCCAGGAAGAAATGAA  360

Query  361  AACTCCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AACTCCTCTGATGTGGTTGGGGGGTCTGCCAGCTGGGGCCCTCCCTGTCGCCAGTGGGCA  420

Query  421  CtttttttttCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGCGAGCAAAGTTCAATAA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTTTTTTTTTCCACCCTGGCTCCTTCAACACGTGCTTGATGCTGCGAGCAAAGTTCAATAA  480
```

```
Query  481  AGATTTTGGGAAGTTT  496
            ||||||||||||||||
Sbjct  481  AGATTTTGGGAAGTTT  496
```

# Sequence 707 matched with Sequence 297

```
Query=   Sequence ID - 707                    nt:      397
Length=397


   SEQ ID NO: 297                    nt:      397

ALIGNMENTS
 Identities = 397/397 (100%), Gaps = 0/397 (0%)

Query  1    CGGATGTGGTGGCAGGCGCCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGGATGTGGTGGCAGGCGCCTCTAGTCCCAGCTACTCGGCAGGCTGAGGTAGGAGAATGG  60

Query  61   CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACTCCAGCCTG  120

Query  121  GGCGGCAGAGCGAGACTCCATCTCaaaaaaaaaaaaaaaaaaaaaTAGACTTTGAGACCAG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGCGGCAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAATAGACTTTGAGACCAG  180

Query  181  CCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAATTACCCGGGCGTGGTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAATTACCCGGGCGTGGTG  240

Query  241  ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACAGGAGAATCACTTGAACCAGG  300

Query  301  GAGGCGGAGGTTGTAGTGAACTGAAATCGTGCCCCTGCACTCCAGCCTGGGTAACAAGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGGCGGAGGTTGTAGTGAACTGAAATCGTGCCCCTGCACTCCAGCCTGGGTAACAAGAG  360

Query  361  CGAAACTCCGTCTCaaaaaataaataaataaataaaat  397
            ||||||||||||||||||||||||||||||||||||||
Sbjct  361  CGAAACTCCGTCTCAAAAAATAAATAAATAAATAAAAT  397
```

# Sequence 708 matched with Sequence 298

```
Query=   Sequence ID - 708                    nt:      293
Length=293


   SEQ ID NO: 298                  nt:      293

ALIGNMENTS
 Identities = 293/293 (100%), Gaps = 0/293 (0%)

Query  1     CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGGGTCC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGGGTCC  60

Query  61    TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCCTTTACAGG  120

Query  121   GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGGCGGGA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTGGGAGGGGCGGGA  180

Query  181   GGGAGGTGTTGCCGTCACTGTATTAAGTCGATGTTGGGAAACGTTTTAACATCTGGAGCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GGGAGGTGTTGCCGTCACTGTATTAAGTCGATGTTGGGAAACGTTTTAACATCTGGAGCC  240

Query  241   TTTGTGGGTGGAAATATGTCTCCAGTTACAACTCCGCAGTGGATGTGAAGAAG    293
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTGTGGGTGGAAATATGTCTCCAGTTACAACTCCGCAGTGGATGTGAAGAAG    293
```

# Sequence 709 matched with Sequence 299

```
Query=  Sequence ID 709
Length=452


   SEQ ID NO: 299

ALIGNMENTS
 Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query  1    GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCATGAAG  60

Query  61   GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAGGAAATTTTGGAGGCAGAAGCTCTGGCCCCTATGGCGGTGGAGGCCAATACTTTGCA  120

Query  121  AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGCTATGGCAGTGGC  180

Query  181  AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG  240
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  181  AGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGCCAGAGAAGTGACAGGG  240

Query  241  AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCACAGTGGTGGCAGGGCCTAGC  300

Query  301  TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCTACAAAGAAGACATGTTTTAGACAAATACTCATGTGTATGGGCAAAAAACTCGAGGA  360

Query  361  CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTGTATTTGTGACTAATTGTATAACAGGTTATTTTAGTTTCTGTTCTGTGGAAAGTGTAA  420

Query  421  AGCATTCCAACAAAGGGGTTTTAATGTANATT   452
            |||||||||||||||||||||||||||||||
Sbjct  421  AGCATTCCAACAAAGGGGTTTTAATGTANATT   452
```

# Sequence 710 matched with Sequence 300

Query=   Sequence ID 710
Length=480


   SEQ ID NO: 300

ALIGNMENTS
 Identities = 480/480 (100%), Gaps = 0/480 (0%)

Query  1    TGGATTCCCGTCGTAACTTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGATTCCCGTCGTAACTTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGTCCTG  60

Query  61   CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACC  120

Query  121  AATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGATGGCATCTATATC  180

Query  181  ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATT  240

Query  241  GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTG  300

Query  301  AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTC  360

Query  361  ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCCAGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACTAACCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCCAGG  420

Query  421  GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCCCTGTGT  480

# Sequence 711 matched with Sequence 301

```
Query=  Sequence ID - 711                    nt:      498
Length=498


   SEQ ID NO: 301                 nt:      498

ALIGNMENTS
 Identities = 498/498 (100%), Gaps = 0/498 (0%)

Query  1    GTGGTACATATACACAAAGGAAAACTATGTAGCCATTAAAAGAAAAGGAACTCCTATCAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGGTACATATACACAAAGGAAAACTATGTAGCCATTAAAAGAAAAGGAACTCCTATCAT   60

Query  61   TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGTAACAACATAAATAAATCTGGAGGAGATTAGGCTAAGGTGAAATAAGCCAGGCACAA   120

Query  121  AAAGACAACTACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAGACAACTACCATATGATCTTACTTATACGTGTGTGGAATCTAAAAAGGTGGAATTTA   180

Query  181  CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTGAGGGCAGGAGGTTGGA   240

Query  241  GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGGATGAATAAGTTCAAGAGATC   300

Query  301  TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATTGTACAACGTGGTGGCTATAGTTGATAACAATGTATTGTGTTCTTGAAAAATGCTGA   360

Query  361  GAGAGTAGATTTTAAGTGTTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGAGTAGATTTTAAGTGTTCTCACCACAAAACATAAGTATGTGAGGTAATGCATGTGTT   420

Query  421  AATTANCTTAATTTAGACATTTCATAATGTATTATACATATTTCAAAACCACGTTGTACA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AATTANCTTAATTTAGACATTTCATAATGTATTATACATATTTCAAAACCACGTTGTACA   480
```

```
Query  481  TGAGAAAGATACACAATT  498
            ||||||||||||||||||
Sbjct  481  TGAGAAAGATACACAATT  498
```

## Sequence 713 matched with Sequence 302

Query= Sequence ID 713
Length=474


   SEQ ID NO: 302

ALIGNMENTS
 Identities = 474/474 (100%), Gaps = 0/474 (0%)

```
Query  1    GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCCAGTCGACCCATGTTCTCCTTTCTACACCAGCATTAGACGCTGTCTTCACAGATTTG  60

Query  61   GAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTGGAGTCTCC  120

Query  121  AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AATCAGTTTCTCATCAACACAAATTCAGAACTTGCTTTGATGTATAATGATGAATCTGTG  180

Query  181  TTGGAAAATCATCACCTTGCTGTGGGTTTCAAACTGCTGCAAGAAGAACACTGTGACATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGGAAAATCATCACCTTGCTGTGGGTTTCAAACTGCTGCAAGAAGAACACTGTGACATC  240

Query  241  TTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGAAGATGGTTATTGACATGGTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGAAGATGGTTATTGACATGGTG  300

Query  301  TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAGCAACTGATATGTCTAAACATATGAGCCTGCTGGCAGACCTGAAGACAATGGTAGAA  360

Query  361  ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACTATACCCGATCGCATTCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACGAAGAAAGTTACAAGTTCAGGCGTTCTTCTCCTAGACAACTATACCCGATCGCATTCA  420

Query  421  GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCCACCAAGTCCTTG    474
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGTCCTTCGCAACATGGTCACTGTGCAGACCTGAGCAACCCCACCAAGTCCTTG    474
```

# Sequence 714 matched with Sequence 303

Query=   Sequence ID 714
Length=535


   SEQ ID NO: 303

ALIGNMENTS
 Identities = 535/535 (100%), Gaps = 0/535 (0%)

```
Query  1    CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAAGCATTATTAGACTTGAAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAAGCATTATTAGACTTGAAAG  60

Query  61   GGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTCAGTTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTTTTCAGTTT  120

Query  121  TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGCAACATTTATATT  180

Query  181  TCTTATTCAGAACCCTTGATGAGACTATTTTTAAACATACTAGTCTGCTGATAGAAAGCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTTATTCAGAACCCTTGATGAGACTATTTTTAAACATACTAGTCTGCTGATAGAAAGCA  240

Query  241  CTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTTCTGTCTGTAACAAAAATGTA  300

Query  301  CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTTATAGAGATGGAGGAAAAGGTCTAATACTACATAGCCTTAAGTGTTTCTGTCATTGT  360

Query  361  TCAAGTGTATTTTCTGTAACAGAAACATATTTGGAATGTTTTTCTTTTCCCCTTATAAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCAAGTGTATTTTCTGTAACAGAAACATATTTGGAATGTTTTTCTTTTCCCCTTATAAAT  420

Query  421  TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTAATTCCTGAAATACTGCTGCTTTAAAAAGTCCCACTGTCAGATTATATTATCTAACA  480
```

```
Query  481  ATTGAATATTGNAAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT  535
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTGAATATTGNAAATATACTTGGCTTACCTCTCAATAAAAGGGTCTTTTCTATT  535
```

## Sequence 717 matched with Sequence 304

```
Query=   Sequence ID 717
Length=464


   SEQ ID NO: 304

ALIGNMENTS
 Identities = 464/464 (100%), Gaps = 0/464 (0%)

Query  1    TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCACCCACCTTGACCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCTCGCCCAGCC  60

Query  61   CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCTAAATAAAT  120

Query  121  ACTGTATTCATAGATTAAAAGACTCAGCATAATAAATATACCATTTCTCCCCAGATTGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACTGTATTCATAGATTAAAAGACTCAGCATAATAAATATACCATTTCTCCCCAGATTGAT  180

Query  181  GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTTGTAGATATGTAAAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTTTGTAGATATGTAAAAG  240

Query  241  ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAATAGATAAAACAAAATGGAGAA  300

Query  301  AGATTTAATAGGAATCACTGTAACTGATTTTAAGACATACAGAACAATAATAGAAACTGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGATTTAATAGGAATCACTGTAACTGATTTTAAGACATACAGAACAATAATAGAAACTGC  360

Query  361  TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTGTATTAGTCCATTTTCACGCTGCTGATAAAGACATACCTGAGATTGGCAATTACAAAG  420

Query  421  GAAAGANGTTTATTGGCTTACAGTTCCCATGGCTGGGGAGGCCT    464
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAAGANGTTTATTGGCTTACAGTTCCCATGGCTGGGGAGGCCT    464
```

# Sequence 718 matched with Sequence 305

```
Query=   Sequence ID 718
Length=588


   SEQ ID NO: 305

ALIGNMENTS
 Identities = 588/588 (100%), Gaps = 0/588 (0%)

Query  1    CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTCATGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTCATGG  60

Query  61   ATCCTGATACCAAACTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCTGATACCAAACTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCAATTCAAAG  120

Query  121  GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCATCTATTACTTCA  180

Query  181  AGGCCAATGTCTTCTTCAAAAACTATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGCCAATGTCTTCTTCAAAAACTATGAAATTAAGAATGAAGCTGATAGGACCTTGATAT  240

Query  241  ATATAACTCTCTACATTTCTGAATGTCTGAAGAAACTGCAAAAGTGCAATTCCAAAAGCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATATAACTCTCTACATTTCTGAATGTCTGAAGAAACTGCAAAAGTGCAATTCCAAAAGCC  300

Query  301  AAGGTGAGAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCCTGGAGAGCCTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGGTGAGAAAGAAATGTATACGCTGGGAATCACTAATTTTCCCATTCCTGGAGAGCCTG  360

Query  361  GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAAACAAACAGGAAGATGAAGTGATGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTTTTCCACTTAACGCAATTTATGCCAAACCTGCAAACAAACAGGAAGATGAAGTGATGA  420

Query  421  GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGCCTATTTACAACAGCTAAGGCAAGAGACTGGACTGAGACTTTGTGAGAAAAGTTTTC  480
```

```
Query  481  GACCCTCAGAATGATAAACCCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACCCTCAGAATGATAAACCCAGCAAGTGGNGGGCTTGCTTTGTGAAGAGACAGTTCATG  540

Query  541  AACAANAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGGCAGCCA  588
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AACAANAGTCTTTCAGGACCTGGACAGTGAAGGGAGCCCGGGCAGCCA  588
```

# Sequence 719 matched with Sequence 306

Query=   Sequence ID 719
Length=492


   SEQ ID NO: 306

ALIGNMENTS
 Identities = 492/492 (100%), Gaps = 0/492 (0%)

Query  1     CGNGGCCGCGTNAACTTTTGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT   63
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CGNGGCCGCGTNAACTTTTGATCGTCAGCTGGGGCTGGCAGGCACCTAAATGGGAAGGGTGAT   63

Query  64    AGCAGTGTGTTGGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT   123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64    AGCAGTGTGTTGGGGGGAGTTTAGGGAACGGTCCTCTACCGATAGAGGCAGCANCTCATT   123

Query  124   GGAATTTCCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC   183
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124   GGAATTTCCTCCTGAAGTTGTCTTGCCCCTTGAATCCTGCAGGAAGGCTGGCAAATGGCC   183

Query  184   ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG   243
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184   ATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATCTGCCCTTAAGACACCACAG   243

Query  244   GACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAGAGGCAGTCCANCTCACCCAACTA   303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244   GACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAGAGGCAGTCCANCTCACCCAACTA   303

Query  304   GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG   363
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304   GGCTCTGCANGGGGACCANGAGGGATGGGTTGTGTCCACAGGACCAGCCAGACTGATGAG   363

Query  364   GGATGCGGCAAGCATATTCTCACCACCTTCTTTCACGTTTACAACANACCAGCNTTCCCT   423
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364   GGATGCGGCAAGCATATTCTCACCACCTTCTTTCACGTTTACAACANACCAGCNTTCCCT   423

Query  424   GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC   483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  424   GTGTGGCAGGGGTTACATTGGTCACCGAGGACCTANAATCATGGAGTGCTCTGGGGATCC   483

```
Query  484  GGGCTTGGA  492
            |||||||||
Sbjct  484  GGGCTTGGA  492
```

Blast comparison trimmed "CGN" from the 5' end of both sequences and reported 489 identities. The report has been manually corrected for this. "CGN" has been prepended to both sequences and identity count has been increased to 492.

# Sequence 720 matched with Sequence 307

Query=   Sequence ID 720
Length=430


   SEQ ID NO: 307

ALIGNMENTS
 Identities = 430/430 (100%), Gaps = 0/430 (0%)

```
Query  1    TCAGTGTTGAATTTTGTCAGACACTTTCTCTGCATCAATTGGTATGACCATGTGAtttttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCAGTGTTGAATTTTGTCAGACACTTTCTCTGCATCAATTGGTATGACCATGTGATTTTTT  60

Query  61   tttCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTTTCAAATAT  120

Query  121  TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGAGCTCTCCTTGCATCTCTGGAATAAGTACCACTTGGTCGTGGTATATATTTCTTTTAA  180

Query  181  TATATTGCTGAATTCTGTTTGATCATGTTTTCTTAAAGACTTTCGTGTCTGTTTTCATGA  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATATTGCTGAATTCTGTTTGATCATGTTTTCTTAAAGACTTTCGTGTCTGTTTTCATGA  240

Query  241  TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTGATTTTGATATCAGGATAATG  300

Query  301  CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTACCTTAATAGAATGAATTGGAGCCAAGTATGGTGGCAAATGCCTATAGTCCTAGCTAC  360

Query  361  TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCAGGAGGCTGAGGTGGTGGGGACTGCTTGACCCANGAGTTCAAATCTAGCTTGGGCAAT  420

Query  421  GTAGCAAGAC    430
            ||||||||||
Sbjct  421  GTAGCAAGAC    430
```

# Sequence 721 matched with Sequence 308

```
Query=   Sequence ID 721
Length=574


   SEQ ID NO: 308


ALIGNMENTS
 Identities = 574/574 (100%), Gaps = 0/574 (0%)

Query  1     TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TAGAAGGAATGACTATTCATGTCCAAAGTGAATGGTTTTGTGCAGTGAACAACACATGGC   60

Query  61    GAGGTACTAACTGAGAAACTTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GAGGTACTAACTGAGAAACTTTTTCATGCTTTATGCCTACCTCTTGTAGTTGTTGCAGAG   120

Query  121   CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAAACTTaaaaa   180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CAAATATAAATTGTAATAAGATAGCTAGGCCTTGCAGAAACAAACAGAAAAACTTAAAAA   180

Query  181   aaaaTGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAAtttttttG   240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAAATGATATAAGAGCTGGAGTCTAGTATTTATATGAATCTGTGAGAGATAATAATTTTTTTG   240

Query  241   GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GTCTCACTGCAATGAACCAAAAGCGGCTGAGTTTGGTTTTTAATTGTAGCCATGTATTGA   300

Query  301   AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGGCATCTTTTTGACCAACTCTTGTTGGTTCTGTCTTGAACCATTGTTAATCACTGTGCT   360

Query  361   GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCCAGCCCACCCCGTCTTCC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTAATTAGTATAGCTAAATCTTTTCCTTCCTTGCTCCTCCCCCAGCCCACCCCGTCTTCC   420

Query  421   CTTAACATTTTTTCAgggggggTTGGGAGTGGTTTCATTTTAATGTGAGTGGATGTTTTG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTTAACATTTTTTCAGGGGGGGTTGGGAGTGGTTTCATTTTAATGTGAGTGGATGTTTTG   480
```

```
Query  481   ATAGTTGTAAGGAAAAAATGCATTTCAGACACATTTCACACATGAGCTATTTTCTTACAC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATAGTTGTAAGGAAAAAATGCATTTCAGACACATTTCACACATGAGCTATTTTCTTACAC   540

Query  541   AGTATGTCTTATTGGTAATAAGAATGTAATTCAT   574
             ||||||||||||||||||||||||||||||||||
Sbjct  541   AGTATGTCTTATTGGTAATAAGAATGTAATTCAT   574
```

# Sequence 722 matched with Sequence 309

```
Query=   Sequence ID 722
Length=327


   SEQ ID NO: 309

ALIGNMENTS
 Identities = 327/327 (100%), Gaps = 0/327 (0%)

Query  1    CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC  62
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCCATCTAC  62

Query  63   TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA  122
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   TCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCAGA  122

Query  123  GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGTCTCaaaaaaaaaaT  182
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  GATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGTCTCAAAAAAAAAAT  182

Query  183  AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG  242
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  AAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCAGCTACCCAGGAGGCTGAG  242

Query  243  GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG  302
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  GCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCATGGAGCTGAGATGGCGCCACTG  302

Query  303  CACTCCAGTCTGGTGACAGAGTGAG   327
            |||||||||||||||||||||||||
Sbjct  303  CACTCCAGTCTGGTGACAGAGTGAG   327
```

Blast comparison trimmed "CN" from the 5' end of both sequences and reported 325 identities. The report has been manually corrected for this. "CN" has been prepended to both sequences and identity count has been increased to 327.

# Sequence 724 matched with Sequence 310

Query=   Sequence ID 724
Length=273


   SEQ ID NO: 310

ALIGNMENTS
 Identities = 273/273 (100%), Gaps = 0/273 (0%)

```
Query  1    CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCCAGCT  60

Query  61   ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGGAGGTTGCG  120

Query  121  GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCaa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAGACTCCGTCTCAA  180

Query  181  aaaaaaaaaaaaaaaaaaaaaaaaaaGACNTCACCTAATTGCAGNGNGNGGACCTTATTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAAAAAAAAAAAAAAAAAAAAAAAGACNTCACCTAATTGCAGNGNGNGGACCTTATTT  240

Query  241  GGCTNTTAATTCAAACTATTAAAAATGTGAACN   273
            |||||||||||||||||||||||||||||||||
Sbjct  241  GGCTNTTAATTCAAACTATTAAAAATGTGAACN   273
```


Blast comparison trimmed "N" from the 3' end of both sequences and reported 272 identities. The report has been manually corrected for this. "N" has been appended to both sequences and identity count has been increased to 273.

## Sequence 726 matched with Sequence 311

```
Query=  Sequence ID - 726                nt:     260
Length=260


   SEQ ID NO: 311                 nt:     260

ALIGNMENTS
 Identities = 260/260 (100%), Gaps = 0/260 (0%)

Query  1    CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCACACCTCCCACCCCCTG  60

Query  61   TATTCCCACCCCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCCATGTGCCTGCAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATTCCCACCCCTGGACTGGTGGCCCCTGCCTTGGGGAAGGTCTCCCCATGTGCCTGCAC  120

Query  121  CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGGAGACAGACAGAGAAGGCAGCAGGCGGCCTTTGTTGCTCAGCAAGGGGCTCTGCCCT  180

Query  181  CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCCCACCTCCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCATACACCCCCACCTCCTG  240

Query  241  CAATAAAATAGTAGCATCGG  260
            ||||||||||||||||||||
Sbjct  241  CAATAAAATAGTAGCATCGG  260
```

## Sequence 727 matched with Sequence 312

Query=   Sequence ID 727
Length=538


   SEQ ID NO: 312

ALIGNMENTS
 Identities = 538/538 (100%), Gaps = 0/538 (0%)

```
Query  1    CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACTCAGTACTGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACTCAGTACTGCA  60

Query  61   GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCTTTCATTCAAATAGGTTATATGTATAAACTGAGTTCAACAATATTGTATTTGAGATGG  120

Query  121  TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAAGTTAAAGAAATGCAATAATGTAAATAATACTTAAGAAAATAAGATCTCAGGAAACT  180

Query  181  GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTCAGTATATGCATCAAGGAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTCAGTATATGCATCAAGGAT  240

Query  241  ATAGTGTATATGACATGAACTTTGAGTGCAAAAACTGTACTATGTACCTTTTGTTTATTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATAGTGTATATGACATGAACTTTGAGTGCAAAAACTGTACTATGTACCTTTTGTTTATTT  300

Query  301  TGCTGTCAACATCTAAATAAAGGtttttttgtttgttttttgtttttttaattgttttgt  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCTGTCAACATCTAAATAAAGGTTTTTTTGTTTGTTTTTTGTTTTTTTAATTGTTTTGT  360

Query  361  tttaaagattgttttaattaattaaaaaattaattgtttttaattaaacaattgtttaatt  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTAAAGATTGTTTTAATTAATTAAAAAATTAATTGTTTTAATTAAACAATTGTTTAATT  420

Query  421  gttttaaaGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTTTTAAAGTCGCCAGGCTGAGGCAGGTGAATCACAAGCTTAGGAGTTGGAGGCTAGCCT  480
```

```
Query  481  GCCAACATGGTGAAACCCCGTCTCTACTAAAAATACaaaaaaaTTAACTGGGTGTGGG  538
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCCAACATGGTGAAACCCCGTCTCTACTAAAAATACAAAAAAATTAACTGGGTGTGGG  538
```

# Sequence 728 matched with Sequence 313

```
Query=   Sequence ID 728
Length=629


   SEQ ID NO: 313

ALIGNMENTS
 Identities = 629/629 (100%), Gaps = 0/629 (0%)

Query  1    CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTTAAATAGTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCATCTGCACCAGTACACAGGCAGGCATTATCATTCTTCACCTACTTTTTAAATAGTGG  60

Query  61   CAACTTGGGATTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAACTTGGGATTCATTCTGGTGATTCTGAACCTTGCCTCATAGCTTAAAGTATAAAAAAG  120

Query  121  ATTCAAGAGCAGTGAGGTTTGTTCTTTCCAGTGAATGGTGGACTGAGTGGTGCGAGGTGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTCAAGAGCAGTGAGGTTTGTTCTTTCCAGTGAATGGTGGACTGAGTGGTGCGAGGTGG  180

Query  181  AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGATGAAAATTCATTTTGA  240

Query  241  AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTATTAAACCAGTGATTACACCTG  300

Query  301  GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTATTGTGATTTTGATGAAGACAGAATT  360

Query  361  ATTTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTTTTCTCTGTAGAAACACAGATACCACTTTATCAGGGGAAGTTAGTCAAATGAAATGG  420

Query  421  AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCCAACATGCTTTAAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAATTGGTAAATGGACAAAAGCTAGCTAGTAAAAAGGACGACCCAGCCAACATGCTTTAAC  480
```

```
Query  481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAACATCTTGAGAAATTTGGGACATAAAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCATTGTATGTTTGTGGAAAGAGCATAGTTTAACATCTTGAGAAATTTGGGACATAAAA  540

Query  541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTTTTCATNGGTAGACAGTTCATGGCAGTATATGAATTGACATAATGGAAATAATCTGAT  600

Query  601  TTTATTTTTACAACTAACATCCTTTCCCC  629
            |||||||||||||||||||||||||||||
Sbjct  601  TTTATTTTTACAACTAACATCCTTTCCCC  629
```

# Sequence 736 matched with Sequence 314

```
Query=   Sequence ID - 736                    nt:     641
Length=641


   SEQ ID NO: 314                 nt:     641

ALIGNMENTS
 Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query  1    GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACT  60

Query  61   TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATAC  120

Query  121  CAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTT  180

Query  181  GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACT  240

Query  241  CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTGGG  300

Query  301  ACTTGAATAAAATTAACCATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATATTTCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACTTGAATAAAATTAACCATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATATTTCAT  360

Query  361  GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAGATCCCACAGT  420

Query  421  TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTGGAGGTCTGTCTGAG  480
```

```
Query  481  CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGC  540

Query  541  TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCTTGATCTTTATCTGTGTCTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGC  600

Query  601  TTCTCAAACTGGAAATGTGCATGTAAGTCACCCANGGGTCT  641
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTCTCAAACTGGAAATGTGCATGTAAGTCACCCANGGGTCT  641
```

# Sequence 739 matched with Sequence 315

Query=   Sequence ID 739
Length=645


   SEQ ID NO: 315

ALIGNMENTS
 Identities = 645/645 (100%), Gaps = 0/645 (0%)

```
Query  1    TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACCCGGG  60

Query  61   AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAAGACTCTGT  120

Query  121  CTCaaaaaaaaaaaaaaaaGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCAAAAAAAAAAAAAAAAGAAATCTTGGGATCCTGAACCCCTTACTCGAAGGGCTAAGG  180

Query  181  TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAGCATCTCAGCATGTCTTATTCGAGACTTCGTANAACCAGACCTGCTGTTTGTAGATGT  240

Query  241  TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTTCTCCTTCTCCGTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTAAGGTTTTCTCCTTCTCCGTA  300

Query  301  TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCACACTTTGGTCTGCTGCTAAGTTGG  360

Query  361  ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCCAGTGTGGGGAGAGGGAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATGCCTCCCACTGTCTTTCCCTAAGTCTAGGGCTTCANACCCCAGTGTGGGGAGAGGGAC  420

Query  421  TTTCGTTTCCTGCCCCTCACCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCGTTTCCTGCCCCTCACCACATCAGACACAGGCAGGCAAGAATAAGATGGCCAAAAG  480
```

```
Query  481  GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCCGATGAACTTCTTGACCTAGCCTGGGACATTACCTGTTACTAGGTGGACTTCACTGCC  540

Query  541  TGTGAATGGAAGCTGAAGGGCTGttttttttGGTTTGTATTTGGACAGGCCAGGCTTANAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGTGAATGGAAGCTGAAGGGCTGTTTTTTTTGGTTTGTATTTGGACAGGCCAGGCTTANAG  600

Query  601  AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC  645
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AGGGAGAGAACTGGGCTACTCTTCAGCAGTGATCTTTAAAATGCC  645
```

# Sequence 747 matched with Sequence 316

Query=   Sequence ID 747
Length=542


   SEQ ID NO: 316

ALIGNMENTS
 Identities = 542/542 (100%), Gaps = 0/542 (0%)

```
Query   1    CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACCATCA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACCATCA   60

Query   61   TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAACCAGGGGG   120

Query   121  AATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGGAGAATAAGAATG   180

Query   181  AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCAGACAAGCAGCTGAGCT   240

Query   241  TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAAGATGCACG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGCCTCCCACGAGAAGATGCACG   300

Query   301  AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAGGCCTCGGGGAGGGCACCCCCTAAG   360

Query   361  ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ACCACAGTGGCCAAGATCACAGTGGCCACGGCCACGGCCACAGTCATGGTGGCCACGGCC   420

Query   421  ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  ACAGCCACTAATCAGGAGGCCAGGCCACCCTGCCTCTACCCAACCAGGGCCCCGGGGCCT   480
```

```
Query  481  GTTATGTCAAACTGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTATGTCAAACTGTCTTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCC  540

Query  541  TC  542
            ||
Sbjct  541  TC  542
```

# Sequence 757 matched with Sequence 317

```
Query=   Sequence ID - 757                    nt:     583
Length=583


    SEQ ID NO: 317                  nt:     583

ALIGNMENTS
 Identities = 583/583 (100%), Gaps = 0/583 (0%)

Query  1     GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGGAAAGaaaa  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGGAAAGAAAA  60

Query  61    aaaaGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTACCGTTCGGA  120

Query  121   CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTACACTGGGCTTCCGTTACAAGA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTACACTGGGCTTCCGTTACAAGA  180

Query  181   TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAGGAGAATGGGTCTCTTG  240

Query  241   TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAGGGTTCGGATGAGACCAGGTG  300

Query  301   TTGCTTGTTCAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TTGCTTGTTCAGTATCTCAAGCCCAGAAAGATGAATTAATCCTTGAAGGAAATGACATTG  360

Query  361   AGCTTGTTTCAAATTCAGCGGCTTTGATTCAGCAAGCCACAACAGTTAAAAACAAGGATA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AGCTTGTTTCAAATTCAGCGGCTTTGATTCAGCAAGCCACAACAGTTAAAAACAAGGATA  420

Query  421   TCAGGAAATTTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTCAGCAGGCTGATG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCAGGAAATTTTTGGATGGTATCTATGTCTCTGAAAAAGGAACTGTTCAGCAGGCTGATG  480
```

```
Query  481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATAAGATCTAAGAGTTACCTGGCTACAGAAAGAAGATGCCAGATGACACTTAAGACCTA  540

Query  541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTTGG  583
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTTGTGATATTTAAATGATGCAATAAAAGACCTATTGATTTGG  583
```

# Sequence 758 matched with Sequence 318

```
Query=   Sequence ID - 758                    nt:     424
Length=424


   SEQ ID NO: 318                 nt:     424

ALIGNMENTS
 Identities = 424/424 (100%), Gaps = 0/424 (0%)

Query  1    CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGGAAGG  60

Query  61   CTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAAGGGAGCAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAAGGGAGCAC  120

Query  121  ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCGAGATGAAACAGAATTCTATTTGGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCGAGATGAAACAGAATTCTATTTGGGC  180

Query  181  AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCACTCCTGGCGGCAAACCA  240

Query  241  AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCCATGGAAACAGTGGCATGGTT  300

Query  301  CGTGCCAAATTCCGAAGCAATCTTCCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CGTGCCAAATTCCGAAGCAATCTTCCTGCTAAGGCCATTGGACACAGAATCCGAGTGATG  360

Query  361  CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTGTACCCCTCAAGGATTTAAACTAACGAAAAATCAATAAATAAATGTGGATTTGTGCTC  420

Query  421  TTGT  424
            ||||
Sbjct  421  TTGT  424
```

## Sequence 764 matched with Sequence 319

```
Query=  Sequence ID - 764                    nt:    626
Length=626


   SEQ ID NO: 319                nt:    626

ALIGNMENTS
 Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query   1    GAttttttttttttttttGAGATGGAGTCTTTCTCTGTCGCCCAGGCTGGAGTGCAGTGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GATTTTTTTTTTTTTTTTTGAGATGGAGTCTTTCTCTGTCGCCCAGGCTGGAGTGCAGTGG   60

Query   61   TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGC   120

Query   121  CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAATTTTTGTATTTTT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAATTTTTGTATTTTT   180

Query   181  AGTAGAGACAGGTTTTCACCATGTTGGCTAGGCTGATTTTGAACTCATGACCCCAAGTGA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGTAGAGACAGGTTTTCACCATGTTGGCTAGGCTGATTTTGAACTCATGACCCCAAGTGA   240

Query   241  TCTGCCCGCCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TCTGCCCGCCTCGGCCTCCCAAAGTGCTGGAATTACAGGTGTGAGCTACCACTCCCAGCC   300

Query   301  AATGATTACATTTATAAGGTAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AATGATTACATTTATAAGGTAAAATAACTTGTGCCAATCTGTACAAGTGAATTCAGATTT   360

Query   361  AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AAAATTTTAATTGTAAAAAGATATCCAGGTGATATTTCTCCCTGAATAATTTAGTTTCCT   420

Query   421  TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TTTCTATTTCTTGATATAAAAGTACTCAGCATTGAAGTAATTGCTATCTTCACATTTCTT   480
```

```
Query  481  CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCCAACACAAAAAACCCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCTATTTGAGCTGTCTAAATAAGTAGTCCTACATATTTTCCCCCCAACACAAAAAACCCA  540

Query  541  GAAAAGAATTATTTTATACTGGAttttttttGGTTGTAGCAGGAACCTAAAGGNGCCAATT  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAAAAGAATTATTTTATACTGGATTTTTTTTGGTTGTAGCAGGAACCTAAAGGNGCCAATT  600

Query  601  GTAACATGCATGTTCTTTTTGGCAAA  626
            ||||||||||||||||||||||||||
Sbjct  601  GTAACATGCATGTTCTTTTTGGCAAA  626
```

## Sequence 766 matched with Sequence 320

```
Query=  Sequence ID 766
Length=618


   SEQ ID NO: 320

ALIGNMENTS
 Identities = 618/618 (100%), Gaps = 0/618 (0%)

Query  1    GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCCCTGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCCCTGA  60

Query  61   TCATTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCATTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCCCTGATCCC  120

Query  121  TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCTGGGGCTGGGCGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCTGGGGCTGGGCGG  180

Query  181  GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTTGGCTGCATCGAAGAGT  240

Query  241  AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAGCAGGAACTCCACTATGCATC  300

Query  301  TCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACCTGACCTCAGGGGCAGAGACAAGAG  360

Query  361  AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGGCACCAAGGAGGATCCAAGAGCTGACTATGCCTGCATTGCTGAGAACAAACCCACCTG  420

Query  421  AGCACCCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGCACCCCAGACACCTTCCTCAACCCAGGCGGGTGGACAGGGTCCCCCTGTGGTCCAGCC  480
```

```
Query  481  AGTAAAAACCATGGTCCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTAAAAACCATGGTCCCCCCACTTCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCC  540

Query  541  GTTCAAAATGATCATCATCAAAACTTATGTGGCTTTTTGACCTTTGAATAGGGAAtttttt  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTTCAAAATGATCATCATCAAAACTTATGTGGCTTTTTGACCTTTGAATAGGGAATTTTTT  600

Query  601  taaaattttttAAAAATT  618
            ||||||||||||||||||
Sbjct  601  TAAAATTTTTTAAAAATT  618
```

# Sequence 768 matched with Sequence 321

Query=   Sequence ID 768
Length=596


   SEQ ID NO: 321

ALIGNMENTS
 Identities = 596/596 (100%), Gaps = 0/596 (0%)

```
Query  1    CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTT  60

Query  61   ttttCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTTAC  120

Query  121  TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAGAGA  180

Query  181  AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCTAAAACAT  240

Query  241  GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAAAGAAAATTGAG  300

Query  301  AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA  360

Query  361  TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT  420

Query  421  GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG  480
```

```
Query  481  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  540

Query  541  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT  596
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT  596
```

# Sequence 773 matched with Sequence 322

Query=  Sequence ID 773
Length=534


   SEQ ID NO: 322

ALIGNMENTS
 Identities = 534/534 (100%), Gaps = 0/534 (0%)

```
Query   1    GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTCAGTTTTACAGATGAAAAGAGTTC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTCAGTTTTACAGATGAAAAGAGTTC   60

Query   61   TGGAGATAGACGGTGTTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTTACCGAACT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TGGAGATAGACGGTGTTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTTACCGAACT   120

Query   121  TAAAAATGTTTAACATAGTATTATGTGATTTTTATTTTGCCACTTaaaaaaaaaGAATGA   180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAAAAATGTTTAACATAGTATTATGTGATTTTTATTTTGCCACTTAAAAAAAAAGAATGA   180

Query   181  AGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTCTGCTCAGTGAAATAAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTCTGCTCAGTGAAATAAG   240

Query   241  CCAGATGCAAAAGATCACATATTATATAATCCACTTATACGAGATACCTAGAATAGGCAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  CCAGATGCAAAAGATCACATATTATATAATCCACTTATACGAGATACCTAGAATAGGCAA   300

Query   301  ATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAGGGGCTGGGGACAAGGGGGCAGTGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAGGGGCTGGGGACAAGGGGGCAGTGA   360

Query   361  GAGATTGAGAGTTATTATTAATGCGTACAGAGTTTCAGTTTGGGCTGATAAAAAAGTTCT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GAGATTGAGAGTTATTATTAATGCGTACAGAGTTTCAGTTTGGGCTGATAAAAAAGTTCT   420

Query   421  GAAGATGGATGGTGATGATGGTTGTACATCAATGTGAGTGTAATTACCGCCACTGAACTG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GAAGATGGATGGTGATGATGGTTGTACATCAATGTGAGTGTAATTACCGCCACTGAACTG   480
```

```
Query  481   CCCTTAAAAACGTTTAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT   534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCCTTAAAAACGTTTAAAAGAGTAAATTTTATGTTGNGTATATTTTACCATAAT   534
```

# Sequence 776 matched with Sequence 323

Query=   Sequence ID 776
Length=556


   SEQ ID NO: 323

ALIGNMENTS
 Identities = 556/556 (100%), Gaps = 0/556 (0%)

```
Query  1    tttttttttCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAGTAGT  60

Query  61   TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGTTTTCCCCC  120

Query  121  ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAAAGTCTCTGGTGA  180

Query  181  TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGGATCTCCCTGAACAAGG  240

Query  241  ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATTTAGCTGCGGGGGTAGCACCC  300

Query  301  TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGATGGGACTGACAGAAGAGAAAAGTTC  360

Query  361  TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCCCAGCCCTTTCTACTTTTTCTCTTTGTTTCTCAGGCTTCTGGCCGTCTTCAGTTTTC  420

Query  421  ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACAAGTTTCACTCTCAACCCTAAACAGTACTTCTGTGAAGTACCCTTTGGCCCCTCGTTT  480
```

```
Query  481   TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TCAGCTCCTAAACTCACCTGGAAATAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAG   540

Query  541   TAGGCATTTTTGGTGA   556
             ||||||||||||||||
Sbjct  541   TAGGCATTTTTGGTGA   556
```

## Sequence 782 matched with Sequence 324

```
Query=   Sequence ID 782
Length=382


   SEQ ID NO: 324

ALIGNMENTS
 Identities = 382/382 (100%), Gaps = 0/382 (0%)

Query  1    CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTACAAAA   60

Query  61   ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTTGAGGAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTTTTGAGGAA   120

Query  121  TAAAATCGCATCATTTCATATGGCTAATGCAattttttttCCCATCTGGAAGCAACATCTG   180
            |||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Sbjct  121  TAAAATCGCATCATTTCATATGGCTAATGCAATTTTTTTTCCCATCTGGAAGCAACATCTG   180

Query  181  ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATGGGAGAGGGTCCGAGAA   240

Query  241  TAGCTCTTCCTGTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAGCTCTTCCTGTTTTCATCAGGACTGTTTTTAGGGATGGCAAAGAAGTCAGTGTGTCCA   300

Query  301  GCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAATCTGCATGTGCANCACNTGCCGTT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAATCTGCATGTGCANCACNTGCCGTT   360

Query  361  GTCTGGGGCATGATCTGTGTGA    382
            ||||||||||||||||||||||
Sbjct  361  GTCTGGGGCATGATCTGTGTGA    382
```

# Sequence 785 matched with Sequence 325

```
Query=  Sequence ID - 785                    nt:    556
Length=556


   SEQ ID NO: 325                nt:    556

ALIGNMENTS
 Identities = 556/556 (100%), Gaps = 0/556 (0%)

Query  1    CTTTTCTCTGGGTATAGATTTACCCTAGCACCTATCTCATTATATTGAATTTTCCAGCAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTTCTCTGGGTATAGATTTACCCTAGCACCTATCTCATTATATTGAATTTTCCAGCAT  60

Query  61   ATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCAACTAATCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCAACTAATCG  120

Query  121  TGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAATACACTGGGACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAATACACTGGGACC  180

Query  181  CAGCATATTGAGTTATATTGGCACAGAAACTTCACTCTGGGTATAGATTTACCCTAGTAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGCATATTGAGTTATATTGGCACAGAAACTTCACTCTGGGTATAGATTTACCCTAGTAC  240

Query  241  CTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAAGGTTCAGGGAAGAGGCTGGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAAGGTTCAGGGAAGAGGCTGGC  300

Query  301  ACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTGAATTCAGCTCAACTCAGCTCCAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTGAATTCAGCTCAACTCAGCTCCAGT  360

Query  361  AGAGATGGTGTCCCCTTCTCTACCGTGTTGAGATAGTGTGCAGTCCCTTCCTAAGGGCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGAGATGGTGTCCCCTTCTCTACCGTGTTGAGATAGTGTGCAGTCCCTTCCTAAGGGCTG  420

Query  421  TTACCCACCGCAATAGGACTTGTCAGCTTCAACTTTTAAATTTCTCTGCTCCCGCTGGGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTACCCACCGCAATAGGACTTGTCAGCTTCAACTTTTAAATTTCTCTGCTCCCGCTGGGA  480
```

```
Query  481   CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCCACCCGCTTCAAAAATCATCATGGNGGNTTTAGCACCAATTTAGTAAACACAAACTGT   540

Query  541   CTGAAATATTTTGGAT   556
             ||||||||||||||||
Sbjct  541   CTGAAATATTTTGGAT   556
```

## Sequence 796 matched with Sequence 326

Query=  Sequence ID 796
Length=716


   SEQ ID NO: 326

ALIGNMENTS
 Identities = 716/716 (100%), Gaps = 0/716 (0%)

```
Query  1    GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCTCTTC  60

Query  61   TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTAGCCCTAAA  120

Query  121  TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTGAATAGCTGGGCC  180

Query  181  TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTGGGCAACTATCTCTAAA  240

Query  241  TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAACTTCATCCTTTGCCGCATCA  300

Query  301  GGACCCTTGATTCCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGACCCTTGATTCCTGAAGAGAACAAGGAGAGGGTACAAGAACTCCCTGATTCTGGAGCC  360

Query  361  CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACTTGGCTTAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCATGCTAGTCCCCAATCGCCAGCTTACTGCTGATTATTTTGAGAAAACTTGGCTTAGC  420

Query  421  CTTAAAGTTGCTCATCAGCAAGTGTTGCCTTGGCGGGGAGAATTCCATCCTGACACCCTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTAAAGTTGCTCATCAGCAAGTGTTGCCTTGGCGGGGAGAATTCCATCCTGACACCCTC  480
```

```
Query   481   CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   CAGATGGCTCTTCAAGTAGTGAACATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGG   540

Query   541   CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG   600
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct   541   CCATGGAAAGCATACCTCAGTGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTG   600

Query   601   CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   CTATTGGAGCCTGGAAACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCG   660

Query   661   GAGACNCTGAATAGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA     716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   GAGACNCTGAATAGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA     716
```

# Sequence 801 matched with Sequence 327

Query=   Sequence ID 801
Length=664


   SEQ ID NO: 327

ALIGNMENTS
 Identities = 664/664 (100%), Gaps = 0/664 (0%)

```
Query   1    CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGC   60

Query   61   GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTAT   120

Query   121  AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGA   180

Query   181  AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACAGCAGAGCAAGGTGCAA   240

Query   241  AACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAACTC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAGACGAGAAATTCTTCCAACTC   300

Query   301  TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAAGAAGAGGAACGAAAAGATGATAAT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAAGAAGAGGAACGAAAAGATGATAAT   360

Query   361  GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGAtttttttGATCCAGTT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GATGATGAGTCAGGTAAAAGTTCCAGAAATGTGAACAACAAAGATTTTTTTGATCCAGTT   420

Query   421  GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GAAAGTGATGAAGACATAGCAAGTGATCATGATGATGAGCTGGGTTCAAACAAGATGATG   480
```

```
Query  481  AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTTCTGAAATATGAATGaaaaaaaTTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAATTGCTGAAGAAGAAGCAGAAGAAGGAAGCATTTCTGAAATATGAATGAAAAAAATTA  540

Query  541  CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGGAAGTGACGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CATCTTTAGAAAAAGAGTTATTAGAAAAAAGCCTTGGCAGCCGTCNGGGGGAAGTGACGC  600

Query  601  ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACAGAAGAGACCAGAGAATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGG  660

Query  661  ATGG  664
            ||||
Sbjct  661  ATGG  664
```

# Sequence 808 matched with Sequence 328

```
Query=   Sequence ID - 808                    nt:     641
Length=641


   SEQ ID NO: 328                nt:     641

ALIGNMENTS
 Identities = 641/641 (100%), Gaps = 0/641 (0%)

Query  1     CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGAAAAT  60

Query  61    GTTAGTATTGCTGCCCTTCTTCACATAAAtttttttttAAATTATACTATTATTTTGCTT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GTTAGTATTGCTGCCCTTCTTCACATAAATTTTTTTTTAAATTATACTATTATTTTGCTT  120

Query  121   AATTTTATATTGGGTTAAAACAACCTTCAAGAAGGTTAACTAGGAAAGAAGACCtttttg  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AATTTTATATTGGGTTAAAACAACCTTCAAGAAGGTTAACTAGGAAAGAAGACCTTTTTG  180

Query  181   ttttatttttACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTTACATGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TTTTATTTTTACTATTTATATATAGAAGACAAATCAGCATTTGGTGATAGTTTTACATGA  240

Query  241   CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTCATTATTAGTAAATTATGTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTTCATTATTAGTAAATTATGTT  300

Query  301   TGATTTTTAAACTATTTAGTACTAATAGTTGAGATGAAAACTGAAGAAAAATGCCAATGT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TGATTTTTAAACTATTTAGTACTAATAGTTGAGATGAAAACTGAAGAAAAATGCCAATGT  360

Query  361   GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GACGTTTGTGTATAGCTAGCCTTAAAAAACTTCCCATGTTTTTAGGTGACTTTTTTCCCC  420

Query  421   CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTCTTAGTACTCTGGAGAAACAATGAAGATGGGCCATCTCAATTCCAGATGTAAACAAAA  480
```

```
Query  481  AGTAATTTTTATTTCAACATTTAATGTAACTGCTATTATTGNGGATTCTTGNCTTGNGTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTAATTTTTATTTCAACATTTAATGTAACTGCTATTATTGNGGATTCTTGNCTTGNGTA  540

Query  541  TTTTCTTTCCCTTATTCAAGTAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTTTCTTTCCCTTATTCAAGTAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGA  600

Query  601  TACGTCATTTCTGTATTGGCAAAATGCCNCTATTAAAGTGT  641
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TACGTCATTTCTGTATTGGCAAAATGCCNCTATTAAAGTGT  641
```

# Sequence 814 matched with Sequence 329

```
Query=   Sequence ID - 814                    nt:     132
Length=132


   SEQ ID NO: 329                 nt:     132

ALIGNMENTS
 Identities = 132/132 (100%), Gaps = 0/132 (0%)

Query  1    GTTAAAGTGATACATTTTTATACCAAATGTGTTTAttttttttGTGCAAGTAATCCTTAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTAAAGTGATACATTTTTATACCAAATGTGTTTATTTTTTTTGTGCAAGTAATCCTTAAA  60

Query  61   ATTGCAATTGTATTAGGTGTtaaaataaagtttttaaaaaattaaaaaaaaaaaaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTGCAATTGTATTAGGTGTTAAAATAAAGTTTTTAAAAAATTAAAAAAAAAAAAAAAAA  120

Query  121  aaaaaaaaaaa  132
            |||||||||||
Sbjct  121  AAAAAAAAAAA  132
```

## Sequence 817 matched with Sequence 330

```
Query=   Sequence ID 817
Length=666


   SEQ ID NO: 330

ALIGNMENTS
 Identities = 666/666 (100%), Gaps = 0/666 (0%)

Query  1    GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGG  60

Query  61   CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCA  120

Query  121  AGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGAGAG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGAGAG  180

Query  181  CCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC  240

Query  241  GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTG  300

Query  301  GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCC  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCC  360

Query  361  TCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAG  420

Query  421  GAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCA  480
```

```
Query  481  CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTaaaaaaaTCCCAAACATATAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  481  CCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAAATCCCAAACATATAAC  540

Query  541  TGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGACTAATGTTAGTATA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGACTAATGTTAGTATA  600

Query  601  AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTAAAACACTGAACTGAC  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AGTAACATGAAAACATTCTTCTNCGCATAAGCCTGCGTCAGATTAAAACACTGAACTGAC  660

Query  661  AATTAA  666
            ||||||
Sbjct  661  AATTAA  666
```

# Sequence 821 matched with Sequence 331

```
Query=  Sequence ID - 821                    nt:     370
Length=370


   SEQ ID NO: 331                  nt:     370

ALIGNMENTS
 Identities = 370/370 (100%), Gaps = 0/370 (0%)

Query  1    AAAGAGCTCCCAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCATCCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAAGAGCTCCCAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCATCCT  60

Query  61   GATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAAT  120

Query  121  ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTC  180

Query  181  ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGT  240

Query  241  ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAATTAATGAAGAAAACAAGCGG  300

Query  301  AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCCTAATGAAATAAATTCACTAAATGG  360

Query  361  ACATTAAAAA   370
            ||||||||||
Sbjct  361  ACATTAAAAA   370
```

# Sequence 825 matched with Sequence 332

Query=  Sequence ID 825
Length=741


   SEQ ID NO: 332

ALIGNMENTS
 Identities = 741/741 (100%), Gaps = 0/741 (0%)

```
Query  1    AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGCCAAT  60

Query  61   TCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGG  120

Query  121  GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG  180

Query  181  CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGC  240

Query  241  GAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCA  300

Query  301  GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGA  360

Query  361  CCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGG  420

Query  421  ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCAT  480
```

```
Query  481   CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAG   540

Query  541   GGAGCCCCCGATTTAAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GGAGCCCCCGATTTAAAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA   600

Query  601   AAAAAGCCAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   AAAAAGCCAAANGGAGCCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAAC   660

Query  661   CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CACCCACACCCCGCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNT   720

Query  721   CTTACNCATNTGTGCNGGNTT   741
             |||||||||||||||||||||
Sbjct  721   CTTACNCATNTGTGCNGGNTT   741
```

Blast comparison trimmed "NGGNTT" from the 3' end of both sequences and reported 735 identities. The report has been manually corrected for this. "NGGNTT" has been appended to both sequences and identity count has been increased to 741.

# Sequence 833 matched with Sequence 333

Query=   Sequence ID 833
Length=719


   SEQ ID NO: 333

ALIGNMENTS
 Identities = 719/719 (100%), Gaps = 0/719 (0%)

```
Query  1    TAAAATAATGGCaaaaaacaaacaaaaaaCAAGTTCTCTAAACAGAAAGGAAATTACTAA  60
            ||||||||||||| ||||| |||| |||||||||||||||||||||||||||||||||||
Sbjct  1    TAAAATAATGGCAAAAAACAAACAAAAAACAAGTTCTCTAAACAGAAAGGAAATTACTAA  60

Query  61   AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATTATGGGTAA  120

Query  121  ATAAAACAGACTTTCCTTCTTTAGTTTCCTAAAATATGTTTGATGATTAATGCAAAAATT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATAAAACAGACTTTCCTTCTTTAGTTTCCTAAAATATGTTTGATGATTAATGCAAAAATT  180

Query  181  ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATATTTAAGATAATTGTACT  240

Query  241  GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACTTTATG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTATACTTCACTCAAACTTTATG  300

Query  301  TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATTAATGTAATCCATAAAGCAACCAAAAAAGCTATACTAAGTACATTCAAAAACACAAT  360

Query  361  AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCaaaaaat  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  361  AGATAAACCAAACAAAATTCTAAAGGATGTACAAGTAACCCACTGGAAGCTGCAAAAAAT  420

Query  421  gtaaacagaaactaaaaacagagaataaatgaaaaattaaaaacgaaatGGCAGACTTAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTAAACAGAAACTAAAAACAGAGAATAAATGAAAAATTAAAAACGAAATGGCAGACTTAG  480
```

```
Query  481   GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GCCCTAATATACAAATTATCACATTAAATATAAATGGTCTAAATACACCAACTGTAAGAC   540

Query  541   AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTC   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGAGATTAGCAAAGTCGATTTAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTC   600

Query  601   ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ACTTCAAATATACCAAGATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATG   660

Query  661   TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT   719
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TGAACATTAATCAAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT   719
```

# Sequence 837 matched with Sequence 334

Query=   Sequence ID - 837                    nt:     603
Length=603


   SEQ ID NO: 334                   nt:     603

ALIGNMENTS
 Identities = 603/603 (100%), Gaps = 0/603 (0%)

```
Query   1    TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCCTGGCTCTTGCCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCCTGGCTCTTGCCC   60

Query   61   TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAGGTACCAAT   120

Query   121  GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACTGCCTTGAAGAAAAAGGACCAATGT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACTGCCTTGAAGAAAAAGGACCAATGT   180

Query   181  TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGGACTGACCTTTTTCCAA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGGACTGACCTTTTTCCAA   240

Query   241  AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTCTGAGGACTACTCTGGATCAG   300

Query   301  GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTGGGAGTGGCTTCCTAACGGAAATGG   360

Query   361  AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCCATGACAACCTTAGGTCTCTTG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AACAGGATTACCAACTAGTAGACGAAAGTGATGCTTTCCATGACAACCTTAGGTCTCTTG   420

Query   421  ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  ACAGGAATCTGCCCTCAGACAGCCAGGACTTGGGTCAACATGGATTAGAAGAGGATTTTA   480
```

```
Query  481  TGTTATAAAAGAGGATTTTCCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TGTTATAAAAGAGGATTTTCCCACCTTGACACCAGGCAATGTAGTTAGCATATTTTATGT  540

Query  541  ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTTAAACATCTGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACCATGGNTATATGATTAATCTTGGGACAAAGAATTTTATAGAAATTTTTAAACATCTGA  600

Query  601  AAA  603
            |||
Sbjct  601  AAA  603
```

# Sequence 839 matched with Sequence 335

```
Query=  Sequence ID - 839                nt:     71
Length=71


   SEQ ID NO: 335              nt:     71

ALIGNMENTS
 Identities = 71/71 (100%), Gaps = 0/71 (0%)

Query  1   ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGaaaaaaaaaaaaaaaaaaaaaaa  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1   ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGAAAAAAAAAAAAAAAAAAAAAAA  60

Query  61  aaaaaaaaaaa  71
           |||||||||||
Sbjct  61  AAAAAAAAAAA  71
```

## Sequence 849 matched with Sequence 336

```
Query=   Sequence ID - 849                    nt:      622
Length=622


   SEQ ID NO: 336                  nt:      622

ALIGNMENTS
 Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query  1     tttttttttatttttttGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTTTTTTTTATTTTTTGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAGTGGT  60

Query  61    GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGTGCTTCAGCCT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGTGCTTCAGCCT  120

Query  121   CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTTGTATTTTTAG  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTTTTGTATTTTTAG  180

Query  181   TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGGCCTAAGTGACCC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGGCCTAAGTGACCC  240

Query  241   ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGTCATTGTCCCCAGCCGGA  300

Query  301   TGTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TGTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTCATCCTCTCCATTTTCTCCTGTTAG  360

Query  361   TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAAACTAAAGTCTCTCTTCCACAAGTCT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TAGTCACAGAGAACCAAATTCTGTCAAGTTATGAAACTAAAGTCTCTCTTCCACAAGTCT  420

Query  421   TCCTGTGTTCTGCCTCAAGTGAACTTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCCTGTGTTCTGCCTCAAGTGAACTTGAAAGAACATCAGTTTGTGGGAAGGTTGAAGACC  480
```

```
Query  481  GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTTCATTTTCAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAATGATCTGCTGGGAAATCACTGAGGCATTGCCATTCTCTTGAGGAATTTCATTTTCAT  540

Query  541  CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CGAAGTTTCGGTTTATATCCCTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATG  600

Query  601  AGTCGTCATCCTTCTTNTGAGC  622
            ||||||||||||||||||||||
Sbjct  601  AGTCGTCATCCTTCTTNTGAGC  622
```

## Sequence 860 matched with Sequence 337

```
Query=  Sequence ID - 860                    nt:     501
Length=501


   SEQ ID NO: 337                 nt:     501

ALIGNMENTS
 Identities = 501/501 (100%), Gaps = 0/501 (0%)

Query   1    GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAACTCAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAACTCAA   60

Query   61   GATTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GATTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCTCACAATAC   120

Query   121  CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGTGCTCTTGGCTCT   180

Query   181  TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAGTCTTTAGTACAAAACTGCTCT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAGTCTTTAGTACAAAACTGCTCT   240

Query   241  AGGGACACCTGGTGATTCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGGGACACCTGGTGATTCCTACACAAGTGATGTTTATATTTCTCATAAAGAGTCTTCCCT   300

Query   301  ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTCAGTGATAACTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATCCCAAGGTCTTCATGATGCCAGTAGCCATATATGATAAATTATGTTCAGTGATAACTT   360

Query   361  AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AGTTATCAGAAATCAGCTCAGTGGTCTTCCCCGCCATGATTCACATTTGATGAGTTTTTA   420

Query   421  AAAATCAAAGTGATTTTGAAAATCTCTAATGGCTCAGAAAATAAAAACATCCAGTTTGTG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AAAATCAAAGTGATTTTGAAAATCTCTAATGGCTCAGAAAATAAAAACATCCAGTTTGTG   480
```

```
Query  481  GATGACTATATTTAGATTTCT  501
            |||||||||||||||||||||
Sbjct  481  GATGACTATATTTAGATTTCT  501
```

# Sequence 864 matched with Sequence 338

Query=  Sequence ID 864
Length=630


   SEQ ID NO: 338

ALIGNMENTS
 Identities = 630/630 (100%), Gaps = 0/630 (0%)

```
Query   1    TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC   60

Query   61   ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG   120

Query   121  ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC   180

Query   181  ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA   240

Query   241  TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAAATGCATACTAATATTTC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAAATGCATACTAATATTTC   300

Query   301  AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG   360

Query   361  AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAGCAATGCATAAGCA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAGCAATGCATAAGCA   420

Query   421  AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCAtttttttttCACAAGATACC   480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCATTTTTTTTTCACAAGATACC   480
```

```
Query  481  TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATGTGAATACAGGGCACCTGGGAGGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540

Query  541  GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCACATACTGATATTGGTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600

Query  601  CAATGTGTAAGGAGATCAGGAATTCATTAG  630
            ||||||||||||||||||||||||||||||
Sbjct  601  CAATGTGTAAGGAGATCAGGAATTCATTAG  630
```

# Sequence 865 matched with Sequence 339

```
Query=  Sequence ID - 865                    nt:     122
Length=122


   SEQ ID NO: 339                 nt:     122

ALIGNMENTS
 Identities = 122/122 (100%), Gaps = 0/122 (0%)

Query  1    CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTCACGA  60

Query  61   GAATAAAGTGTCAAGCAAGaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  120

Query  121  aa  122
            ||
Sbjct  121  AA  122
```

# Sequence 867 matched with Sequence 340

Query=   Sequence ID 867
Length=640


   SEQ ID NO: 340

ALIGNMENTS
 Identities = 640/640 (100%), Gaps = 0/640 (0%)

```
Query  1    ttttttttttttttttttttCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTTTTTTTTTTTTCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTTTACA   60

Query  61   ACTTTTCAGACACAAGTAAGTACATAAATATTATTTTACAACCAACAATNTTTAATATTT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTTTCAGACACAAGTAAGTACATAAATATTATTTTACAACCAACAATNTTTAATATTT   120

Query  121  CCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAAAAAGACATGAAA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAAAAAGACATGAAA   180

Query  181  CATAAACCTAATTATACATAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATAAACCTAATTATACATAAAAGAAAAGAATTTTAAACAAGAGCTTATTGNGATGACAT   240

Query  241  TACTCATAACTTTTACCTTTAAAACCTTTTCTTGGGTAGCTATTCAAAAGTAAAGACCAC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACTCATAACTTTTACCTTTAAAACCTTTTCTTGGGTAGCTATTCAAAAGTAAAGACCAC   300

Query  301  AAGTTTTGTTGCCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGTTTTGTTGCCCANATTTCTTATGTTTNGTATATTTAAGCTCTTTATTTATTGAACAG   360

Query  361  ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGAtttttttttCCC   420
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  361  ATGNGTCATTAATTCATTNGGAGCATTACTATTATCAGTAAAATTTGATTTTTTTTTCCC   420

Query  421  CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTTAGTCAATAT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTCAGTCATAGGTAAATCAGCTCCACCTGGAATTTCTAAGGACCCAGTTTTAGTCAATAT   480
```

```
Query  481  TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTTCAAGTAATCATGACCTCAGAAATAGTCTTAATTAAGATAACAAATATTAGCCATCAA  540

Query  541  AATGGAACCAAGACAAGATTCTAATGTTTGTAAACAGTCAATCCATATTTATGAATATTA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AATGGAACCAAGACAAGATTCTAATGTTTGTAAACAGTCAATCCATATTTATGAATATTA  600

Query  601  GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG  640
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GCATATATTGGNGAATAGTTAAGGCAAAAGGGTCTAGCAG  640
```

# Sequence 869 matched with Sequence 341

```
Query=  Sequence ID - 869                    nt:     667
Length=667


   SEQ ID NO: 341                 nt:     667

ALIGNMENTS
 Identities = 667/667 (100%), Gaps = 0/667 (0%)

Query  1     TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATATCTGC  60

Query  61    ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGAAACTATTG  120

Query  121   ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATCATTTAATAGGAC  180

Query  181   ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGGCTGTACTCTAAAATAA  240

Query  241   TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAAATGCATACTAATATTTC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTCAAAATGCATACTAATATTTC  300

Query  301   AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATCTACTTGTGATAGCCCTAAGAGCTG  360

Query  361   AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAGCAATGCATAAGCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AGATAATTATTTCCAGGAGGTTGAATCCCTGATTCTTAACTGTTCAGCAATGCATAAGCA  420

Query  421   AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCAtttttttttCACAAGATACC  480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AGAGAGAATATGACATAAGAGGACCATTTCTACATTAGCCATTTTTTTTTCACAAGATACC  480
```

```
Query  481  TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TATGTGAATACAGGGCACCTGGGANGGTAAGTGGAGGACTATTTCTAACTATATTTATAA  540

Query  541  GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCACATACTGATATTGNTGAATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGA  600

Query  601  CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CAATGTGTAAGGAGATCAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGC  660

Query  661  TGTACCG  667
            |||||||
Sbjct  661  TGTACCG  667
```

## Sequence 870 matched with Sequence 342

```
Query=   Sequence ID 870
Length=591


   SEQ ID NO: 342

ALIGNMENTS
 Identities = 591/591 (100%), Gaps = 0/591 (0%)

Query  1    GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGCTCAA  60

Query  61   GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCCGGCCTTCT  120

Query  121  GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAAGGCCAAGATGTT  180

Query  181  AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCCCATGGATCCTGCTCTC  240

Query  241  CGATGACAAGGGAGACCATCCCCCACCCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGATGACAAGGGAGACCATCCCCCACCCCCGGAGTCCAAAATACAGAGTTTCTTTGGCCT  300

Query  301  ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGAGACCAGCAGCCCTGCACCCAGCAA  360

Query  361  GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCTAGGGGGAGAAGAGGAGGCCCAACCACAGTCTCCAGCTCCTGATCCGCCCTGTTCTGC  420

Query  421  CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCTCCACGAACACCTTTGTCTGGGGGCCTCAGCCGCCCCAGAGGCCTGACTTAGGGGTCT  480
```

```
Query  481   GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GGCTGTGGAAGGATGTGTGGCCTCAAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGC   540

Query  541   CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC   591
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAGGGGTCTGCCCCAATCCTGGCCTGCATCAGGCAAGGACGGGGTCTCAGC   591
```

# Sequence 871 matched with Sequence 343

```
Query=  Sequence ID - 871                  nt:     642
Length=642


   SEQ ID NO: 343              nt:     642

ALIGNMENTS
 Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query  1    GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATGAAAA  60

Query  61   AGAAACATTAACTGCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGAAACATTAACTGCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCAAAGTACAG  120

Query  121  CAGGCGGGAAAAGAAAATGGTAGAttttttttCTTCCAATTACTTTAACTTATTCTTTTTA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGGCGGGAAAAGAAAATGGTAGATTTTTTTTCTTCCAATTACTTTAACTTATTCTTTTTA  180

Query  181  ATGGACACTTcatacataaatatattcacaatatattaatatatacataatgtataagca  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGGACACTTCATACATAAATATATTCACAATATATTAATATATACATAATGTATAAGCA  240

Query  241  tacatatTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TACATATTGAATGTGCAGTCAAAAAATGTACTAATGGAATGCTCTACCAAAACAAGTTCA  300

Query  301  CGTTCATCTGTAAAATGGGAATAATATTTTTAAAAGGCATACAGTCTGAACATTTTTAGA  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CGTTCATCTGTAAAATGGGAATAATATTTTTAAAAGGCATACAGTCTGAACATTTTTAGA  360

Query  361  TTATTCATAAAATCTATTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTATTCATAAAATCTATTCAGAAAGTTAAACTAAAAAATTTAACGTATGCCTATAACAAA  420

Query  421  TTTTGTACTTAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTTGTACTTAATGTAATTGNTTTTCATCCTGAGATCTAATATCCTCGTTTTTAAGTAGA  480
```

```
Query   481  GCCACTTGTTTGCTACAGTTTAGTCAAAACGTTAACATTAGATGGGTAAAGTAATATGAA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GCCACTTGTTTGCTACAGTTTAGTCAAAACGTTAACATTAGATGGGTAAAGTAATATGAA   540

Query   541  ATCTTTCTACTACTCCAAAATAGAAAACAGAACATTAAAAAGATAAAAATTCAAACATAC   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATCTTTCTACTACTCCAAAATAGAAAACAGAACATTAAAAAGATAAAAATTCAAACATAC   600

Query   601  TTACCAGTAGATTTTCAACTGNGCAAAAGCTCATTGCATGGG   642
             ||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TTACCAGTAGATTTTCAACTGNGCAAAAGCTCATTGCATGGG   642
```

## Sequence 873 matched with Sequence 344

Query=  Sequence ID 873
Length=661


   SEQ ID NO: 344

ALIGNMENTS
 Identities = 661/661 (100%), Gaps = 0/661 (0%)

```
Query  1    GTTTTCCACCGTGAAGAGAACATTTCCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTTCCACCGTGAAGAGAACATTTCCTCTGGGAATGACAAAGCCCTCAGGAACNGCTTT  60

Query  61   TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAATTTATTTAT  120

Query  121  TCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTACGTTTTATAGAAG  180

Query  181  CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTAATCTAGTCAGAATATC  240

Query  241  CTTATCCTTCTAAAATAAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTATCCTTCTAAAATAAAACTAGTTAAAATTATTAACATACGTACTGATATTAATTTTT  300

Query  301  AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACATTTATCACTACAAGTGGCAGAAAAT  360

Query  361  TCCAAACTCATCAAAACCAAACTGTTGCTTCTTCCCTGCTTTTTCAGAAAATGAGAAAGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCCAAACTCATCAAAACCAAACTGTTGCTTCTTCCCTGCTTTTTCAGAAAATGAGAAAGG  420

Query  421  ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATGACTTTATTCCAACATATTCTAAAAGTATTCCAAGAACACTACCTTTATTCTAAATTC  480
```

```
Query  481   GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GTTATTTTCACAAAATAAAGGCTGCAGATTGAAAGATAAAGGATTGCTATTAAAGAACAA   540

Query  541   AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCanaanaaCCGAATAN   600
             |||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||
Sbjct  541   AAGAAAACAAAACCGAGAGAGAAGGAGAGCTAGGGAAATCCCTGCANAANAACCGAATAN   600

Query  601   GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GGTCCCTCTATTCTGGGCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGC   660

Query  661   A   661
             |
Sbjct  661   A   661
```

## Sequence 875 matched with Sequence 345

Query=   Sequence ID 875
Length=661


   SEQ ID NO: 345

ALIGNMENTS
 Identities = 661/661 (100%), Gaps = 0/661 (0%)

```
Query   1    CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGGGAGG   60

Query   61   CAGCCGGCACCCACAAGTGCCACTGCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CAGCCGGCACCCACAAGTGCCACTGCCCGAGCTGGTGCATTACAGAGAGGAGAAACACAT   120

Query   121  CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGTGAAACACACCAG   180

Query   181  GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAAGTCCTTACCTCTTCCG   240

Query   241  GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGTGACACTTCANAGAGCTGGTA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGTGACACTTCANAGAGCTGGTA   300

Query   301  GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTCTTTTCTCTTTCTCCTTAGTCTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTCTCTCTTTTCTCTTTCTCCTTAGTCTT   360

Query   361  CTCATAGCATTAACTAATCTATTGGGTTCATTATTGGAATTAACCTGGTGCTGGATATTT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTCATAGCATTAACTAATCTATTGGGTTCATTATTGGAATTAACCTGGTGCTGGATATTT   420

Query   421  TCAAATTGTATCTAGTGCAGCTGATTTTAACAATAACTACTGTGTTCCTGGCAATAGTGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TCAAATTGTATCTAGTGCAGCTGATTTTAACAATAACTACTGTGTTCCTGGCAATAGTGT   480
```

```
Query  481  GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTCTGATTAGAAATGACCAATATTATACTAAGAAAAGATACGACTTTATTTTCTGGTAG  540

Query  541  ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATAGAAATAAATAGCTATATCCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGN  600

Query  601  AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AATGTTACTGATCATGCATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCA  660

Query  661  T  661
            |
Sbjct  661  T  661
```

# Sequence 876 matched with Sequence 346

```
Query=  Sequence ID - 876                    nt:     115
Length=115


   SEQ ID NO: 346                 nt:     115


ALIGNMENTS
 Identities = 115/115 (100%), Gaps = 0/115 (0%)

Query  1    AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTTCCCAATAAATTAAGAGC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTTCCCAATAAATTAAGAGC  60

Query  61   CAAATTGTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa   115
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAAATTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   115
```

# Sequence 878 matched with Sequence 347

```
Query=   Sequence ID - 878                  nt:     634
Length=634


  SEQ ID NO: 347                 nt:     634

ALIGNMENTS
 Identities = 634/634 (100%), Gaps = 0/634 (0%)

Query  1    GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGGCACT   60

Query  61   GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTCAC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTTGCTTTCAC   120

Query  121  AGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAACCGCCAAGTCCAA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAACCGCCAAGTCCAA   180

Query  181  AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGCTGATCCGCCTCCACTT   240

Query  241  CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCagaaggt   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATACAGGGGTGCATTGCAGAAGGT   300

Query  301  cagagagaaggagctggaagaagaaaagaagaagaaATCCTGGGATTTTGGGGCTTTCCA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGAGAGAAGGAGCTGGAAGAAGAAAAGAAGAAGAAATCCTGGGATTTTGGGGCTTTCCA   360

Query  361  ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCCAGCTCGGCAACAGACTCTTCCATGGAGGAGATCTTTCAGCACCTGATGGCCTATCA   420

Query  421  CCAGGAGGCCAGCAAGCGCATCTCCAGCCACACTCCCTTTGATCATCCAGTTCTTCATGCT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCAGGAGGCCAGCAAGCGCATCTCCAGCCACACTCCCTTTGATCATCCAGTTCTTCATGCT   480
```

```
Query  481   CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCAGACGTACGGCCAGCAGCTTCAAAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACA   540

Query  541   CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG   600
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  541   CCTACAGCTGGCTCCTGAAGGAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGG   600

Query  601   AGCGGCTTGCACGGCTGACGCAGGCTCGGCGCCG   634
             ||||||||||||||||||||||||||||||||||
Sbjct  601   AGCGGCTTGCACGGCTGACGCAGGCTCGGCGCCG   634
```

# Sequence 879 matched with Sequence 348

Query=  Sequence ID 879
Length=528


   SEQ ID NO: 348

ALIGNMENTS
 Identities = 528/528 (100%), Gaps = 0/528 (0%)

```
Query  1    GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTTTTCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTTTTCA  60

Query  61   CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGCAGCTGCCTCATTTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATACCTCCACG  120

Query  121  TTCTCGCCAACACTTGTTGTTGTCTGTAATTTCGTTGTTAGCCATCCCAGTGGGGATGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCTCGCCAACACTTGTTGTTGTCTGTAATTTCGTTGTTAGCCATCCCAGTGGGGATGAA  180

Query  181  GTAGTATCTTACTGTGGTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTAGTATCTTACTGTGGTTTTCAGTTGCGTTTCCCTGATAATTAATGATGGTGAACATCT  240

Query  241  TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGaaaaaaaaaaTGTCTGTTCAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGAAAAAAAAAAATGTCTGTTCAAA  300

Query  301  TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCTTTACAAAGTATTTATTTTTTATGTCAACAATATAACCACTCAGTACACTGCTTTTT  360

Query  361  ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAATTTTAAGGTTATG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ANACAATGATCTTTTAAAGGTTTGTTTACAACATTTAGCACTTGAAATTTTAAGGTTATG  420

Query  421  CCCTCaaaaaaaTTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCCTCAAAAAAATTGCTGAGGGAGCTAAGCTATGAAGATGCAAAGGCATAANAATTATAC  480
```

```
Query  481  AATGGACTTTGGGGGAATCCAGGGAAAGGGTGGGAGGGGGGTGANGGA  528
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATGGACTTTGGGGGAATCCAGGGAAAGGGTGGGAGGGGGGTGANGGA  528
```

## Sequence 881 matched with Sequence 349

```
Query=   Sequence ID 881
Length=573


   SEQ ID NO: 349

ALIGNMENTS
 Identities = 573/573 (100%), Gaps = 0/573 (0%)

Query  1    TCGACTCTGAttttttttttCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGGNGCGCGG  60
            ||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCGACTCTGATTTTTTTTTTCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGGNGCGCGG  60

Query  61   CCCCTGTCCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCCCTGTCCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACATCCTCCTGG  120

Query  121  CCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACACAAGCAAAGTTT  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACACAAGCAAAGTTT  180

Query  181  ATTCCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACTCCAAATTAAGGAAGGTGAAAT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTCCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACTCCAAATTAAGGAAGGTGAAAT  240

Query  241  ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAATAAGTACTTAAAAGGTAAAG  300

Query  301  TAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATGTCTACAAAGAACATTTCCAAGATG  360

Query  361  ATGTCTTTAATGAAAAGGGATGGAACTACATTCTTGAGAAGTATGATGGGCATCTTCCAA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATGTCTTTAATGAAAAGGGATGGAACTACATTCTTGAGAAGTATGATGGGCATCTTCCAA  420

Query  421  TANAAATAAAAGCTGTTCCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TANAAATAAAAGCTGTTCCTGAGGGCTTTGTCATTCCCAGAGGAAATGTTCTCTTCACGG  480
```

```
Query  481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTGTTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TGGAAAACACAGATCCAGAGTGTTACTGGCTTACAAATTGGATTGAGACTATTCTTGTTC  540

Query  541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
            |||||||||||||||||||||||||||||||||
Sbjct  541  AGTCCTGGTATCCAATCACAGTGGCCACAAATT  573
```

## Sequence 883 matched with Sequence 350

Query=   Sequence ID 883
Length=659


   SEQ ID NO: 350

ALIGNMENTS
 Identities = 659/659 (100%), Gaps = 0/659 (0%)

```
Query  1    TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCATTTT  60

Query  61   GCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAGGCCTTAAG  120

Query  121  ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTTGTTCTACCCTTT  180

Query  181  AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGGGTGAGGGCCCAAGGAC  240

Query  241  CTTTCAAACTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCCTCTGTCGAAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTTCAAACTCAGATCTCTTATTTAATAACCTGGTCCCAGATCCATTCCTCTGTCGAAGA  300

Query  301  GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTTAAGAGCGCAGACTATGAATTCAGT  360

Query  361  CTTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTTTTTGGGTCCCAGTTTGCCAGACCTTGAGTGAGTGCCCCGAGTTTACTTACTTGTAAA  420

Query  421  GGTAGGTGGAGGtaatataattaaataaacttaaaaaactaattaaaaacaaaacaaatG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGTAGGTGGAGGTAATATAATTAAATAAACTTAAAAAACTAATTAAAAACAAAACAAATG  480
```

```
Query  481  AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACTAAGGTCTTAGGATATCTGGCGTCTATTTTGCGCCAAATCACATAATGTCTATTGTT  540

Query  541  GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTGTGTTGGACTATAGGATTGTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCT  600

Query  601  GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA  659
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GTCAATATTATGACCATGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA  659
```

# Sequence 885 matched with Sequence 351

Query=  Sequence ID 885
Length=517


   SEQ ID NO: 351

ALIGNMENTS
 Identities = 517/517 (100%), Gaps = 0/517 (0%)

```
Query   1    TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCTGCCT   60

Query   61   GCCATCGCTGTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GCCATCGCTGTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGAGAGAAAAA   120

Query   121  TCCCGGTGCTTGGTGTCCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAAATGT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TCCCGGTGCTTGGTGTCCTTGCATGACATGGAGTTTTGCATGTAGATCAATTTAAAATGT   180

Query   181  ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTGCCAAACTTTGGAAATG   240

Query   241  TTAATGTTCANACTGAAAATCTCCACTACATGTAACTTTCTTCCTCTGGATCAGTGGCAT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTAATGTTCANACTGAAAATCTCCACTACATGTAACTTTCTTCCTCTGGATCAGTGGCAT   300

Query   301  GGCTTATAATCCCAGCCAGTGGTTTGAACTGTTCCAGTGTCAACTGCCATGTGCTCTGCT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGCTTATAATCCCAGCCAGTGGTTTGAACTGTTCCAGTGTCAACTGCCATGTGCTCTGCT   360

Query   361  TCAAGGGGGAACTAGCCTTTTGTGAATTTTTTGTACATAAGTATTTGTTACAAATATTTT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TCAAGGGGGAACTAGCCTTTTGTGAATTTTTTGTACATAAGTATTTGTTACAAATATTTT   420

Query   421  AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AGCAAATGCTTTCTATTTCTCTTGCTTGTGCATATCTTGGCTGGCGTTACAGAAAAATAG   480
```

```
Query  481   TGTAAACATTATTTCCTTACCGGGGAATGAGGGTTTT   517
             |||||||||||||||||||||||||||||||||||||
Sbjct  481   TGTAAACATTATTTCCTTACCGGGGAATGAGGGTTTT   517
```

# Sequence 887 matched with Sequence 352

```
Query=   Sequence ID 887
Length=174


   SEQ ID NO: 352

ALIGNMENTS
 Identities = 174/174 (100%), Gaps = 0/174 (0%)

Query  1    AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGTTTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGTTTTC  60

Query  61   ACTTTGAATCTCTCTTGAGTATTGTTCTCCTTATTGATTACATGATGACATCCTGTTTTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTTGAATCTCTCTTGAGTATTGTTCTCCTTATTGATTACATGATGACATCCTGTTTTC  120

Query  121  TCTCCCTGACCTTTACTGTTTGTTTAGaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  174
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTCCCTGACCTTTACTGTTTGTTTAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  174
```

# Sequence 889 matched with Sequence 353

```
Query=  Sequence ID 889
Length=664


   SEQ ID NO: 353

ALIGNMENTS
 Identities = 664/664 (100%), Gaps = 0/664 (0%)

Query  1    CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACACAGA  60

Query  61   GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACTCTCGCTGCTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACTCTCGCTGCTGG  120

Query  121  CGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGAAACAAATTTCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGAAACAAATTTCTG  180

Query  181  TTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTGAGAACACAGCTGTACN  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTGAGAACACAGCTGTACN  240

Query  241  ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATTATNAGGGAAACAGAAAACACTGATACTTAACAATGCTAATGCAATTATTTATTTGCT  300

Query  301  TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAATATTTGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTCAGTCTCTACAAAACGTTCTAAAACACTAATCTAAATATTAACAGTAAAATATTTGC  360

Query  361  ATAACTAATGGAAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATAACTAATGGAAACTAAGAAATCATATGACCAATATTTCACTTATTGGTAATCTTACTC  420

Query  421  TACTGATTTCCCCCCAGACTGTGATTTTTGAACTTCCTTGCCTTTCTCCTGTCTTTCTGN  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACTGATTTCCCCCCAGACTGTGATTTTTGAACTTCCTTGCCTTTCTCCTGTCTTTCTGN  480
```

```
Query  481  GTTTATTCATGGAATTCCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTATTCATGGAATTCCAGTTATCTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCA  540

Query  541  AAATCTGACAGATCAGCAAAATGAGATAAATGTTTCTTTTTTCTTTCTGACTGCATTAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAATCTGACAGATCAGCAAAATGAGATAAATGTTTCTTTTTTCTTTCTGACTGCATTAAA  600

Query  601  TCAGATACAACTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TCAGATACAACTCAGCATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGT  660

Query  661  CTTA  664
            ||||
Sbjct  661  CTTA  664
```

## Sequence 890 matched with Sequence 354

Query= Sequence ID 890
Length=661


   SEQ ID NO: 354

ALIGNMENTS
 Identities = 661/661 (100%), Gaps = 0/661 (0%)

```
Query  1    CCAGTTCCACATTCAGTGAAGTCATGAACTTGAAATTGGCCATGATCAAAAAGTATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAGTTCCACATTCAGTGAAGTCATGAACTTGAAATTGGCCATGATCAAAAAGTATTTAA  60

Query  61   ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTTCTCTTGGAGAACCTGTTAAAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCACAGAAGTTGCAAATGCCACAAATCAAGGTCTTTTTCTCTTGGAGAACCTGTTAAAC  120

Query  121  ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTTACCAACTCACGACCGCCATGCACCCAATACTGCAATAGGTCTATAGATGCAGATAC  180

Query  181  TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAGTCCTACCAGAAGAACA  240

Query  241  TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCCAAAGATGTCCACATCCTAATC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCCAAAGATGTCCACATCCTAATC  300

Query  301  CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAAGGGACTTTGCCACAGGTTTTTAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTGAAGCCTATGAATATACTACTTTACTTGGCAAAAGGGACTTTGCCACAGGTTTTTAA  360

Query  361  TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAATCCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTAAGGACCTTGAAATAGAGAGATTATCCTGGATAATCCAGATGGCCCCAGTGTAATCCC  420

Query  421  AAGGGTCCTCACAAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGGGTCCTCACAAAGGGTAGGAAGGAGAGCCAGAGTCAGAGAAGGAGACGTAGCAATGG  480
```

```
Query  481   AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AGGCAGAGGTCANAGAGAGATCTGCAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATG   540

Query  541   CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAGGTGACCTCAANGNGCTAGATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGG   600

Query  601   ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ATGGGCATTATTATGAGTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATG   660

Query  661   C   661
             |
Sbjct  661   C   661
```

# Sequence 891 matched with Sequence 355

```
Query=   Sequence ID - 891                    nt:     626
Length=626


   SEQ ID NO: 355               nt:    626

ALIGNMENTS
 Identities = 626/626 (100%), Gaps = 0/626 (0%)

Query  1     GGCAGAGGTTGCAGTGAACTGAGATCATGCCATTGCAATCCAGCCTGGGCAACANGAGTG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGCAGAGGTTGCAGTGAACTGAGATCATGCCATTGCAATCCAGCCTGGGCAACANGAGTG  60

Query  61    AGACTCCATCTCaaaaaaaaaaaaaaaaaaGACAAGAGTNTCCACTCTAAACACTTNTATT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AGACTCCATCTCAAAAAAAAAAAAAAAAAAGACAAGAGTNTCCACTCTAAACACTTNTATT  120

Query  121   CAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGCAATAAAATGTAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGCAATAAAATGTAT  180

Query  181   TCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATATAATTCTCTACCTGGGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATATAATTCTCTACCTGGGA  240

Query  241   AACTTCACCGAAAAAGATTTCACCAAAAGATTTCTAAGCCTAAATAATGACTTCAGCAAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACTTCACCGAAAAAGATTTCACCAAAAGATTTCTAAGCCTAAATAATGACTTCAGCAAA  300

Query  301   GTCTCACCATACAAAATCAACATACACAAATGAGTAGCATTTCTGTGCACCAATAATATT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GTCTCACCATACAAAATCAACATACACAAATGAGTAGCATTTCTGTGCACCAATAATATT  360

Query  361   CAAGCTGAGaaaaaaaGAACATGGTTCTATTTACAATAGCTACAAACaaaaaaaTATGTA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CAAGCTGAGAAAAAAAGAACATGGTTCTATTTACAATAGCTACAAACAAAAAAAATATGTA  420

Query  421   CCTAGTAATACATTAAATCAAGGNGGTAAAATATCTNTACAACAAGAACTACAAAACTGC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CCTAGTAATACATTAAATCAAGGNGGTAAAATATCTNTACAACAAGAACTACAAAACTGC  480
```

```
Query  481  TGaaaaaaaaTAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TGAAAAAAAATAGAGACACGCAAATAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAG  540

Query  541  AATCAATATAATTAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTC  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AATCAATATAATTAAAATGTCCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTC  600

Query  601  TCTCAAACTATAAATGCACCTTTTTA  626
            ||||||||||||||||||||||||||
Sbjct  601  TCTCAAACTATAAATGCACCTTTTTA  626
```

# Sequence 893 matched with Sequence 356

```
Query=   Sequence ID - 893                    nt:     585
Length=585


   SEQ ID NO: 356                  nt:     585

ALIGNMENTS
 Identities = 585/585 (100%), Gaps = 0/585 (0%)

Query  1     GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTCATTGCTGGGTGGCGCCAGCCCTCAGACTTGCCTCTTTGCAGTAGGAAGAAGGCCTCC   60

Query  61    CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAATATGACCA   120

Query  121   TCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAATGTGGTGGGTAA   180

Query  181   ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCTGGCACTGCTACTTACT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCTGGCACTGCTACTTACT   240

Query  241   AGTGAATTTAAGCAAGTTATTTCACCTTTCAGAGTGTCAGTTCCCTCATGCATACAAGGA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AGTGAATTTAAGCAAGTTATTTCACCTTTCAGAGTGTCAGTTCCCTCATGCATACAAGGA   300

Query  301   AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGAGAACTACATGTA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGATAAAAAATAATGTNTACNAAAGTATTGGAGTAATTAATACATGGAGAACTACATGTA   360

Query  361   AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AAGCGTTTAGCATGATGTCTGACATATTAAGCATCCAATATTAGTNGCTTGCAGAATTAT   420

Query  421   TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAGTAAAAGAGATTGCTTCTGAAAGCCATTCCAATTCTTAAATTTTATAATGCCACATTT   480
```

```
Query  481  GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTTGCGATTTATTTTTTCAATTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGGTCACCTGAAGTCGTGTATAACATGTGTACATTTTTGCGATTTATTTTTTCAATTCC  540

Query  541  CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG  585
            |||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  541  CANATTAAAGGCATAGAGATATCCTAGCNANGGACTCCAAGTGTG  585
```

# Sequence 895 matched with Sequence 357

Query=   Sequence ID - 895                    nt:      560
Length=560


   SEQ ID NO: 357                  nt:      560

ALIGNMENTS
 Identities = 560/560 (100%), Gaps = 0/560 (0%)

```
Query  1     GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGGaaaaaaaaaagaaaaaaaa  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGGAAAAAAAAAAGAAAAAAAA  60

Query  61    CTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGTAAATGGGG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGTAAATGGGG  120

Query  121   CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAGGGTTCCTTTGAC  180

Query  181   TCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGGCTTTCTCAGGCAAGTA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGGCTTTCTCAGGCAAGTA  240

Query  241   GCAGGGTGGCTACTATGTATCGCTTCTTTAttttttttctttttttAAAATAATGCAGGCACC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GCAGGGTGGCTACTATGTATCGCTTCTTTATTTTTTTCTTTTTTAAAATAATGCAGGCACC  300

Query  301   GTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTTaaaaaaaaaaaGCTGTTCTCATCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTTAAAAAAAAAAAGCTGTTCTCATCT  360

Query  361   CCTGTCtttctttttttttttctttttatttttttctttttattattattatactttaagtt  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCTGTCTTTCTTTTTTTTTTTCTTTTTATTTTTTTCTTTTTATTATTATTATACTTTAAGTT  420

Query  421   ttaGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCATGTNGGT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCATGTNGGT  480
```

```
Query  481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATccctccc  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGCTGCACCCATTAACTCGTCATTTAGCATTAGGTATATCTCCTAATGCTATCCCTCCC  540

Query  541  ccctcccccctttttttttt  560
            ||||||||||||||||||||
Sbjct  541  CCCTCCCCCCTTTTTTTTTT  560
```

# Sequence 896 matched with Sequence 358

Query= Sequence ID 896
Length=645


   SEQ ID NO: 358

ALIGNMENTS
 Identities = 645/645 (100%), Gaps = 0/645 (0%)

```
Query  1    GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGGAATGTCTTAGGCACTGGGACTGTAAGTGCAAAGACCCTGTGGCACAAGGGAATGTTA  60

Query  61   ATTATCTACCTTTCANAAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAACAATAAGGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTATCTACCTTTCANAAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAACAATAAGGG  120

Query  121  AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAAttttttt  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTTAAAAATTTTTTT  180

Query  181  aaaaaaaTCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTaaaaaanaTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  181  AAAAAAATCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTTGACTTTTAAAAANATT  240

Query  241  ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTAGTTTANATGATAATGGCATT  300

Query  301  CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAGATATTCCANAATTGAGGGATTTGT  360

Query  361  GAGGTGAAATCATTTGTTACAGATATTAAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGGTGAAATCATTTGTTACAGATATTAAAGGATAAGGAGCTTTGTCAAAGGGGATCTTA  420

Query  421  AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTTTCTGGTATGGTAACTGGGTTAGAGAGCCCTGGAACATGACCAGCTTTAAGGGAAGA  480
```

```
Query  481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGCTTGAGCTCTGTTCTTGTTAAGCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAG  540

Query  541  GTCTAAGCAGGGAACTGGCTTGGCTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTCTAAGCAGGGAACTGGCTTGGCTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATA  600

Query  601  TGGTAATTATTAATAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
            |||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  601  TGGTAATTATTAATAAAAGCCTTAGGTANATGAAATTGTTTTGGG  645
```

## Sequence 897 matched with Sequence 359

```
Query=   Sequence ID - 897                    nt:     509
Length=509


   SEQ ID NO: 359                nt:     509

ALIGNMENTS
 Identities = 509/509 (100%), Gaps = 0/509 (0%)

Query  1     GCAAATCTACACATTTGATTAAATGATAGGGAACTATGCACACACATAATACATATAATG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCAAATCTACACATTTGATTAAATGATAGGGAACTATGCACACACATAATACATATAATG  60

Query  61    CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTGGGGGAAAC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTGGGGGAAAC  120

Query  121   TGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTATGTGAATCTATA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTATGTGAATCTATA  180

Query  181   ATTATTCCAAAATAAAAAGTTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTATTCCAAAATAAAAAGTTTTAAAGAACCTAAGTATCCTTATTACTGAGGGTCATCGT  240

Query  241   GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAAATACTAAATACCAGCCTGG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAAAATACTAAATACCAGCCTGG  300

Query  301   GCAACATAGCAAGACCCTGCCTCTACaaaaagcaaaaaaaTTAGCTGGGCATGGTGGTAC  360
             |||||||||||||||||||||||||||      |||||||| |||||||||||||||||||
Sbjct  301   GCAACATAGCAAGACCCTGCCTCTACAAAAAGCAAAAAAAATTAGCTGGGCATGGTGGTAC  360

Query  361   ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATGCCTGTGGTCCTAGTTACTCTTGGAGGAGTCTGAGGTGGGGAGCTTGAGCCTAGGAGT  420

Query  421   TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TTGAGGCCGCAGTGAGCCTTGATTGTGTCTCTGTACTCCAGTCTGGGCCACAGAGCAAGA  480
```

```
Query  481  CCCGGTCTCTAAAAATAAATAAATAAATA  509
            |||||||||||||||||||||||||||||
Sbjct  481  CCCGGTCTCTAAAAATAAATAAATAAATA  509
```

## Sequence 898 matched with Sequence 360

Query= Sequence ID 898
Length=511


   SEQ ID NO: 360

ALIGNMENTS
 Identities = 511/511 (100%), Gaps = 0/511 (0%)

```
Query  1    ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTaaaaaaaaaaaaaaaaaaaaaa  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTAAAAAAAAAAAAAAAAAAAAAA  62

Query  63   aGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTTCCCACAACT  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   AGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTTTCCCACAACT  122

Query  123  CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  CACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCCCTTTCAACGCACAC  182

Query  183  ACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  ACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGGCAGATACTGTTGAGTCCC  242

Query  243  TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  TGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCTTCTGCTTAATGACCATCTCGAA  302

Query  303  GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303  GTAACAAGTTTAGCCTAAAATAAACTTGCTAAGTTAGCAAAGGAAGTCCTTAGCAGCCAC  362

Query  363  CATTTCTCGATTCCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA  422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363  CATTTCTCGATTCCTCCATCACCTCCCCTGCCCCTCAACTCCCTCATTTCTCCCAAGATA  422

Query  423  TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG  482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423  TGGGCTCCAGGCTGGGCGCGGTGGCTCACGCCTATAATCCTAGCACTTTGGGAGGCTGAG  482
```

```
Query  483  GTGAGCAGATCACTGAGGTCAGGAGTTCG  511
            |||||||||||||||||||||||||||||
Sbjct  483  GTGAGCAGATCACTGAGGTCAGGAGTTCG  511
```

Blast comparison trimmed "AN" from the 5' end of both sequences and reported 509
identities. The report has been manually corrected for this. "AN" has been prepended to
both sequences and identity count has been increased to 511.

# Sequence 899 matched with Sequence 361

```
BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.




Query=   Sequence ID 899
Length=16


   SEQ ID NO: 361                                    26.3    2e-06

ALIGNMENTS
 Identities = 16/16 (100%), Gaps = 0/16 (0%)

Query  1    TCNTTCGGAACGCGCC  16
            ||||||||||||||||
Sbjct  1    TCNTTCGGAACGCGCC  16
```

Blast comparison trimmed "TCN" from the 5' end of both sequences and reported 13
identities. The report has been manually corrected for this. "TCN" has been prepended to
both sequences and identity count has been increased to 16.

## Sequence 900 matched with Sequence 362

Query=  Sequence ID 900
Length=579


    SEQ ID NO: 362

ALIGNMENTS
 Identities = 579/579 (100%), Gaps = 0/579 (0%)

```
Query  1    CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACTTAGTAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACTTAGTAC  60

Query  61   CTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTCAGAGAATAGCAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTCAGAGAATAGCAAG  120

Query  121  TATTCTAGTTTGAGTGGCCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTCTAGTTTGAGTGGCCACCTGGTACGTATATAAGGGAATAGTAAAAGATCTGGCTGGA  180

Query  181  AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAACTGGAACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGACTGTGGAACTGGAACT  240

Query  241  TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCTAATTAGAGTTGATATTTAGG  300

Query  301  AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAACTGAGTGAGACTAGTACTGGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTCAAACTGAGTGAGACTAGTACTGGA  360

Query  361  GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GACTGGTTAAGAGACTACAACAATAACCTGAGTAAGAATTAATACAGGCCTGACCTAGTT  420

Query  421  TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTGAGTGAGTAGGATTGGAAACAAGAGTTTTAGGTATTATAGGATTTATGCATATAAAAT  480
```

```
Query  481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAAGGACACAGAAAGTGAGGCAGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGACTTGACAGAACTTGAAGAAAGAGAAAGTGTCAAAAGGACACAGAAAGTGAGGCAGGA  540

Query  541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
            |||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATCTTACAATGTTAAAGGAAAGGAATAATAGAAGTTAC  579
```

# Sequence 903 matched with Sequence 363

```
Query=   Sequence ID 903
Length=185


   SEQ ID NO: 363

ALIGNMENTS
 Identities = 185/185 (100%), Gaps = 0/185 (0%)

Query  1    GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACATATCT  60

Query  61   CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCATCAGACTTTGTACCCTCTCTCTTCCATCCCTTACCCTTACCGATTAGGTTGGTATTA  120

Query  121  CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAAGGTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTACCCCATAAGGTA  180

Query  181  TAATT  185
            |||||
Sbjct  181  TAATT  185
```

# Sequence 904 matched with Sequence 364

Query=   Sequence ID 904
Length=649


   SEQ ID NO: 364

ALIGNMENTS
 Identities = 649/649 (100%), Gaps = 0/649 (0%)

```
Query  1    CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAAAGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAAAGTG  60

Query  61   AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAGCCAAGTGG  120

Query  121  AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTCAGGAAGGGGATA  180

Query  181  TAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGGGAGTGCAAAGGGAAGG  240

Query  241  TGGGCATTTTCCCCAAAGTTTTTGTTGAAGACTGCGCAACTACAGATTTGGAAAGCACTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGGCATTTTCCCCAAAGTTTTTGTTGAAGACTGCGCAACTACAGATTTGGAAAGCACTC  300

Query  301  GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGCTGAAGAAAATGAAGCCCTATTACT  360

Query  361  TGTTTGTAAGATTTAGCACCCTTCTGCTGTATACTGTACTGAGACATTACAGTTTGGAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGTTTGTAAGATTTAGCACCCTTCTGCTGTATACTGTACTGAGACATTACAGTTTGGAAG  420

Query  421  TGTTAACTATTTATTCCCTGTTAAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTTAACTATTTATTCCCTGTTAAAATTTAACCTACTAGACAATGATGTGAGTACCCAGG  480
```

```
Query  481  ATGATTTCCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGATTTCCTGGGGCACAGTGGGTGAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGG  540

Query  541  AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAAGTCTTCCAGGTCTGATC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGAGGAAAAGTGGATGGAAGTGTCTGGAAAGGGCACCAAAAAAGTCTTCCAGGTCTGATC  600

Query  601  CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACATN  649
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CTGTTTCTTGCTCTGAGTGCTAGCTACCACTGTGTCACACTGTAACATN  649
```

Blast comparison trimmed "N" from the 3' end of both sequences and reported 648 identities. The report has been manually corrected for this. "N" has been appended to both sequences and identity count has been increased to 649.

# Sequence 905 matched with Sequence 365

```
Query=   Sequence ID - 905                    nt:     655
Length=655


   SEQ ID NO: 365                  nt:     655

ALIGNMENTS
 Identities = 655/655 (100%), Gaps = 0/655 (0%)

Query  1    CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACCCACA  60

Query  61   TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTAAACAAGCA  120

Query  121  GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCATTTCCCAGGGGT  180

Query  181  ACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATGTGAATAGCAAAAGTAG  240

Query  241  GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAAGACTGCTGTCCGCCTCCAGG  300

Query  301  CCtgcatgcacacacccatgcccacctgcacccccagcaccacgcccacactcactcgca  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTGCATGCACACACCCATGCCCACCTGCACCCCCAGCACCACGCCCACACTCACTCGCA  360

Query  361  cacacccacatgccaGTGTTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAACACAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CACACCCACATGCCAGTGTTTTGGGGTTGGCAGCCTGGACACTGCTGAGGCAAACACAAG  420

Query  421  TCATCAAGCATAATTCTCATTCTCTCCTTCTGTGTCTCTGTTTTAGTTACAGGAATTTGGTC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TCATCAAGCATAATTCTCATTCTCTCCTTCTGTGTCTCTGTTTTAGTTACAGGAATTTGGTC  480
```

```
Query  481  AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGTTTAGAGGATTTAATAAGTCCGTGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGA  540

Query  541  AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAGTAAGTGCATGCTTCATGATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCAC  600

Query  601  TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT  655
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGGCCANGGCCTGGCCCGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT  655
```

# Sequence 906 matched with Sequence 366

Query=   Sequence ID 906
Length=334


   SEQ ID NO: 366

ALIGNMENTS
 Identities = 334/334 (100%), Gaps = 0/334 (0%)

```
Query  1    CAGAATTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAATTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTGGACG   60

Query  61   ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAATGATATCAG   120

Query  121  TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTGCTTGTGTGCTTG   180

Query  181  GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCAATGATCTCTGCAAGTT   240

Query  241  CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGCCGCCAGAGTTGCTGCTTACT   300

Query  301  GGATGCGTAAGAAGAAAAGaaaaaaaaaaaaaaa   334
            |||||||||||||||||||||||||||||||||
Sbjct  301  GGATGCGTAAGAAGAAAAGAAAAAAAAAAAAAAA   334
```

## Sequence 907 matched with Sequence 367

```
Query=   Sequence ID - 907                    nt:    582
Length=582


   SEQ ID NO: 367                  nt:    582

ALIGNMENTS
 Identities = 582/582 (100%), Gaps = 0/582 (0%)

Query  1     CTTCCATTGGGGGTAAAGATCAAACTTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTCCATTGGGGGTAAAGATCAAACTTTAGGCGAGCCAGGTCTGTATCTCCATTCCTGTC   60

Query  61    TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCCACAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTTGTCCACAA   120

Query  121   GTCTATGCTCTAACTCTGTCACCTGCATGGCTGCAAATTAGCTTCCTTCTTCCTGCCCTC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTCTATGCTCTAACTCTGTCACCTGCATGGCTGCAAATTAGCTTCCTTCTTCCTGCCCTC   180

Query  181   TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTGTAC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGATGTCCGTGTGTGTGTAC   240

Query  241   TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCTTCAAATGTAAGTCATTTTGG   300

Query  301   CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTTTGGGAGGCTGAGGTGAGCTGATCA   360

Query  361   TTTGAGGTTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACTCCATCTCTACCAAA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TTTGAGGTTAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACTCCATCTCTACCAAA   420

Query  421   AATACAAAAATTAGCTGGGTATGGTAGTGCACGCCTGTAATCCCAGCTACTTGGAATGCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AATACAAAAATTAGCTGGGTATGGTAGTGCACGCCTGTAATCCCAGCTACTTGGAATGCT   480
```

```
Query  481  GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAGCAGGAGAATTGCCTGAACCCANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCA  540

Query  541  CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAAA  582
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTGCACTCCAACCTGGGTGACAGAGCAAGGCTGTGTCTCAAA  582
```

# Sequence 908 matched with Sequence 368

Query=  Sequence ID 908
Length=530


   SEQ ID NO: 368

ALIGNMENTS
 Identities = 530/530 (100%), Gaps = 0/530 (0%)

```
Query  1    ACCTGACTTCAAACTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGTACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCTGACTTCAAACTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGTACAA  60

Query  61   AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAAACTGCACATCTACAACCATC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAAACTGCACATCTACAACCATC  120

Query  121  TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCTATTTAATAAATG  180

Query  181  GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAAACTGGACCCCTTCCTTACACC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGCTGGGAGAACTGGCTAGCCATGTGCAGAAAATTGAAACTGGACCCCTTCCTTACACC  240

Query  241  TTATACAAAAATTAACTCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTATACAAAAATTAACTCAAGATGGATTAAAGACTTAAATGTAGAACCCAAAACGATAAA  300

Query  301  AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACCCTAGAAGAAAATCTAGGCAATATCATTAAGGACATAGACATGGGCAAAAATTTCAT  360

Query  361  GATGAAAACATCAAAAGCAATGGCAACAAAAGCAGAAACTGACAAATGGGCTTCTGCACA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATGAAAACATCAAAAGCAATGGCAACAAAAGCAGAAACTGACAAATGGGCTTCTGCACA  420

Query  421  GCAAAAGAAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCAAAAGAAACTATCGTCAGAGTGAACAGACAACCTACAGAATGGGAGACAGTTTTTGCA  480
```

```
Query  481   ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTTAA   530
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATCTATCCATCTGACAAAAGTCTAATATCCAGAATCTACAAGGAATTTAA   530
```

# Sequence 910 matched with Sequence 369

Query=  Sequence ID 910
Length=653


   SEQ ID NO: 369

ALIGNMENTS
 Identities = 653/653 (100%), Gaps = 0/653 (0%)

```
Query   1    CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCAGGAG   60

Query   61   GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGAGCCATGAT   120

Query   121  CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAAACTTGGTCCCTCGCAAAATGTTG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAAACTTGGTCCCTCGCAAAATGTTG   180

Query   181  AAGCCCAGTTTTCACTATTAACCTGTATTTCAGTTTCCCCATGCTAACTTTGAAACACTG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AAGCCCAGTTTTCACTATTAACCTGTATTTCAGTTTCCCCATGCTAACTTTGAAACACTG   240

Query   241  GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACTCAGTAATTTAAACTTAAAATCCTAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACTCAGTAATTTAAACTTAAAATCCTAA   300

Query   301  GGAACTTCAAAAAGTGTAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTTGCTTGT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGAACTTCAAAAAGTGTAATCTAGTCCAAATGGGGCATCAATTCTAAAGCATTTGCTTGT   360

Query   361  TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTTATGACTAAATCCA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TTGAGCAGATTTTCTGTGTCTGAGGTATATAGATAACTTATCTTTTTATGACTAAATCCA   420

Query   421  AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AGTCCTTAGTTCCTGTTGGAATTCAAAATCATATTTAAAAATTGATGCTTTGTTCTATAA   480
```

```
Query  481   TTAATGCTTTGATTGTATAAATAATAAGTATTCTTCCAAATCCCTTTTTACAGATGATGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TTAATGCTTTGATTGTATAAATAATAAGTATTCTTCCAAATCCCTTTTTACAGATGATGA   540

Query  541   TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TTCTGATACCGAGACGTCAAATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAA   600

Query  601   CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC   653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CAGAAATCAGAACTACCTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC   653
```

# Sequence 911 matched with Sequence 370

```
Query=   Sequence ID - 911                    nt:      595
Length=595


   SEQ ID NO: 370                   nt:      595

ALIGNMENTS
 Identities = 595/595 (100%), Gaps = 0/595 (0%)

Query  1     GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCCTGCTGTGCCANAAACCCTTAAGAAAAAG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GAGGGTGTAGAAGAGAAGAAGAAGGAGGTTCCTGCTGTGCCANAAACCCTTAAGAAAAAG  60

Query  61    CGAAGGAATTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAAGATG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CGAAGGAATTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCCAAAAGATG  120

Query  121   CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTATCACAAGGAATAT  180

Query  181   AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAGAAAAGCTGGCAACTTC  240

Query  241   TATGTACCTGCAGAACCCAAATTGGCGTTTGTCATCAGAATCAGAGGTATCAATGGAGTG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TATGTACCTGCAGAACCCAAATTGGCGTTTGTCATCAGAATCAGAGGTATCAATGGAGTG  300

Query  301   AGCCCAAAGGTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGCCCAAAGGTTCGAAAGGTGTTGCAGCTTCTTCGCCTTCGTCAAATCTTCAATGGAACC  360

Query  361   TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TTTGTGAAGCTCAACAAGGCTTCGATTAACATGCTGAGGATTGTAGAGCCATATATTGCA  420

Query  421   TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TGGGGGTACCCCAATCTGAAGTCAGTAAATGAACTAATCTACAAGCGTGGTTATGGCAAA  480
```

```
Query  481  ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCAATAAGAAGCGAATTGCTTTGACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAA   540

Query  541  TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGGAAAAC   595
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TACNGCATCATCTGCATGGAGGATTTGATTCATGAGATCTATACTGTTGGAAAAC   595
```

# Sequence 912 matched with Sequence 371

```
Query=   Sequence ID - 912                  nt:     651
Length=651


   SEQ ID NO: 371                 nt:     651

ALIGNMENTS
 Identities = 651/651 (100%), Gaps = 0/651 (0%)

Query  1    CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTAGAAT   60

Query  61   GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACAAAAATTAT   120

Query  121  AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTAAAAATTAAAACCAAGTGTTG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTAAAAATTAAAACCAAGTGTTG   180

Query  181  TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGGAGATTATTTTGTTATT   240

Query  241  TAAAATTAAAGTGGCTGTGTAGTTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAAAATTAAAGTGGCTGTGTAGTTTTAACTTTAGTATTGCAGGTAGAGTAAGCTTACATG   300

Query  301  ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATAACAAAAATCTTGGTCTTAGTGACTTAATGATTCTGATATTTATTGATTGATTGGTTA   360

Query  361  TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCATTCCAAATATTTTAAAAGATAATAGCTGGCTGGGTGCGGTGGCTCATGCCTGTAATC   420

Query  421  CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCAGCACTTTGGGAGGCCAGGACGGGCGGATCACGAGGTCAGGAGATCAAGACCATCCTG   480
```

```
Query  481  GCTAACACGGTGAAACCCCGTCTCTACTaaaaatcaaaaaaTTAGCCGGGTGTAGTGGCG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCTAACACGGTGAAACCCCGTCTCTACTAAAAATCAAAAAATTAGCCGGGTGTAGTGGCG  540

Query  541  GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGCACCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAG  600

Query  601  GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA  651
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GCGGAGCTTGCAGTGAGCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA  651
```

# Sequence 913 matched with Sequence 372

Query=  Sequence ID 913
Length=531


    SEQ ID NO: 372

ALIGNMENTS
 Identities = 531/531 (100%), Gaps = 0/531 (0%)

```
Query  1    GTGAGGTGGGGACTTCATTCATTGTCCTATTTCTATCTCCACTTTGTGCCTGGAGAGCTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGAGGTGGGGACTTCATTCATTGTCCTATTTCTATCTCCACTTTGTGCCTGGAGAGCTT  60

Query  61   TCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACCCACTATAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACCCACTATAC  120

Query  121  CCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCATTAAAGTTGTTTGAACCAAAGTGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCATTAAAGTTGTTTGAACCAAAGTGG  180

Query  181  CGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATCATCCGCTCGCCCTCCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATCATCCGCTCGCCCTCCT  240

Query  241  TTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGGGGGTGACTCGCCATGCTTGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGGGGGTGACTCGCCATGCTTGG  300

Query  301  CACCCTCTGCTTCCTGGTGCTGCTCTGACTCGAAGACGGGACAGTCCCTGGTGCACATCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACCCTCTGCTTCCTGGTGCTGCTCTGACTCGAAGACGGGACAGTCCCTGGTGCACATCC  360

Query  361  AGGGAAGAGGAGTGTCGGTAGTTCTTGCAGTAGGCACTTTATCAGGACCTGACCTGTTGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGGGAAGAGGAGTGTCGGTAGTTCTTGCAGTAGGCACTTTATCAGGACCTGACCTGTTGC  420

Query  421  TGGGTGATTTTAGTCTCTACAAACAGAAAGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGGTGATTTTAGTCTCTACAAACAGAAAGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAG  480
```

```
Query  481   TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTTATCTCT   531
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TGACCCTTTGCTGATGCTGGGGGGAGGGGATCTAAATCCTCATTTATCTCT   531
```

## Sequence 914 matched with Sequence 373

Query=   Sequence ID 914
Length=602


   SEQ ID NO: 373

ALIGNMENTS
 Identities = 602/602 (100%), Gaps = 0/602 (0%)

```
Query  1    GGCGCCTGCTGGAGGAGGAGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGACTGGAGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCGCCTGCTGGAGGAGGAGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGACTGGAGG  60

Query  61   CCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTG  120

Query  121  GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGC  180

Query  181  CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  181  CTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGG  240

Query  241  AATAATCAGGCTTTTTAAATGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATAATCAGGCTTTTTAAATGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAGC  300

Query  301  AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGGGTTCTCTGTCCCTGGTTCAACTGT  360

Query  361  GATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTGTGGGTTTGGGT  420

Query  421  GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGC  480
```

```
Query  481  TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGTGTGAACCGTGTGGACAGTGGTGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTC  540

Query  541  CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCTGGCTGTTGAGGCGCTGCTTTAACCTGCACCCCTNCCTTGCTCATANATGCTCCTTTT  600

Query  601  GA  602
            ||
Sbjct  601  GA  602
```

# Sequence 915 matched with Sequence 374

```
Query=  Sequence ID - 915                    nt:     230
Length=230


   SEQ ID NO: 374                nt:     230

ALIGNMENTS
 Identities = 230/230 (100%), Gaps = 0/230 (0%)

Query  1    TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTAG  60

Query  61   CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTAGGAGAATC  120

Query  121  GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCATTGCACTCCAGCC  180

Query  181  TGGGCGACAGAGCGAGACTCCATCTaaaanaaaaTAAATGAATAAAATAA   230
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGGCGACAGAGCGAGACTCCATCTAAAANAAAATAAATGAATAAAATAA   230
```

# Sequence 917 matched with Sequence 375

```
Query=   Sequence ID 917
Length=483


   SEQ ID NO: 375

ALIGNMENTS
 Identities = 483/483 (100%), Gaps = 0/483 (0%)

Query  1     NNCAGAtttttttttttttttttCAGNGTTAGACCATCTTTCAATTCCTGGAACAAACTTAACT  62
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     NNCAGATTTTTTTTTTTTTTTTTCAGNGTTAGACCATCTTTCAATTCCTGGAACAAACTTAACT  62

Query  63    TTCCATGATATGtattttttatacattgctggattttatttgctaatatttttacttagga  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63    TTCCATGATATGTATTTTTTATACATTGCTGGATTTTATTTGCTAATATTTTACTTAGGA  122

Query  123   tttaattttCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTTGTCACATTTTAG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   TTTAATTTTCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCATTTGTCACATTTTAG  182

Query  183   TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183   TATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGTTTATGTAANATAAAGTAC  242

Query  243   ATTTCTTCTAAAGGTTTGNGTGGATTAACTTTCAAATCTGCCANAGNGNGtttttttcct  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243   ATTTCTTCTAAAGGTTTGNGTGGATTAACTTTCAAATCTGCCANAGNGNGTTTTTTTCCT  302

Query  303   ttttttttttttttCATTTNAAGGGAGNGCAAGTANCttttcaaatnctgatttaatttt  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   TTTTTTTTTTTTTTCATTTNAAGGGAGNGCAAGTANCTTTTCAAATNCTGATTTAATTTT  362

Query  363   taaaatatttncaagtntntttanagtttttatttnttntngaangttaacatttttata  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   TAAAATATTTNCAAGTNTNTTTANAGTTTTTATTTNTTNTNGAANGTTAACATTTTTATA  422

Query  423   naaaanGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423   NAAAANGGTNTTATCTTTTTAAATTCTTTGACATCAGTTTCTTCANAATTCCTTCTTTTA  482
```

```
Query  483  A  483
               |
Sbjct  483  A  483
```

Blast comparison trimmed "NN" from the 5' end of both sequences and reported 481 identities. The report has been manually corrected for this. "NN" has been prepended to both sequences and identity count has been increased to 483.

# Sequence 926 matched with Sequence 376

Query=  Sequence ID 926
Length=538


   SEQ ID NO: 376

ALIGNMENTS
 Identities = 538/538 (100%), Gaps = 0/538 (0%)

```
Query  1    GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCAGGGC  60

Query  61   CCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCATCGTGGGC  120

Query  121  ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTACTGTG  180

Query  181  ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGGGGTCTGGGTTTTCTTG  240

Query  241  TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCTGCCTCATTACTGGGAAGCAG  300

Query  301  CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATCCACACAGGGGCTAACGCAGCCTGGGACCCTGTGTGCCAGCACTTACTCTTTTGTGC  360

Query  361  AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTTGGGGTCCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGCACATGTGACAATGAAGGACGGATGTATCACCTTGATGGTTGTGGTGTTGGGGTCCTG  420

Query  421  ATTTCAGCATTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATTTCAGCATTCATGAGTCAGGGGAAGGTCCCTGCTAAGGACAGACCTTAGGAGGGCAGT  480
```

```
Query  481   TGGTCCAGGACCCACACTTGCTTTCCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG   538
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TGGTCCAGGACCCACACTTGCTTTCCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG   538
```

## Sequence 938 matched with Sequence 377

```
Query=   Sequence ID 938
Length=440


   SEQ ID NO: 377

ALIGNMENTS
 Identities = 440/440 (100%), Gaps = 0/440 (0%)

Query  1    TGGCCATCCTTTTCCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGCCATCCTTTTCCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCCCGAC  60

Query  61   CCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAGGAGGTGGT  120

Query  121  TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCCTCCATCCTGCTT  180

Query  181  ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGGGGCCAGGACTGGGTCA  240

Query  241  CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGCCCCTGCAGTTCCCAGTCTCT  300

Query  301  TCTGTCCTGCAGCCCTTGCCTCTTTCCCACAGGTTCCACTTTATATCCACCttttccttt  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCTGTCCTGCAGCCCTTGCCTCTTTCCCACAGGTTCCACTTTATATCCACCTTTTCCTTT  360

Query  361  tgttcaattttttattttttattttttttATTATTAAATGATGTGGTCTATGGaaaaaaaaa  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGTTCAATTTTTATTTTTATTTTTTTTATTATTAAATGATGTGGTCTATGGAAAAAAAAAA  420

Query  421  taaaaaTCTGACTTAGTTTT  440
            ||||||||||||||||||||
Sbjct  421  TAAAAATCTGACTTAGTTTT  440
```

# Sequence 939 matched with Sequence 378

```
Query=   Sequence ID - 939                    nt:      513
Length=513


   SEQ ID NO: 378                  nt:     513

ALIGNMENTS
 Identities = 513/513 (100%), Gaps = 0/513 (0%)

Query  1     GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGTGAAT  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGTGAAT  60

Query  61    ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAATTCTCTAA  120

Query  121   CACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACATGTGGGGGACAC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACATGTGGGGGACAC  180

Query  181   ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCATGCCCTACCCTCTGGG  240

Query  241   GGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATTTAACTTCTGTCCTAGGGAAA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATTTAACTTCTGTCCTAGGGAAA  300

Query  301   ACAGTGTCTGATGAGGAGTGTTTCCAACACAGGCTACATGAATTCCCCTATACCAGTGCG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ACAGTGTCTGATGAGGAGTGTTTCCAACACAGGCTACATGAATTCCCCTATACCAGTGCG  360

Query  361   AAAGCAGCCAGGAGTCCCCGTTGGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AAAGCAGCCAGGAGTCCCCGTTGGAAAAGAACAATGCCACTCTCTTTTATGTATCTTGGT  420

Query  421   TCTGCAACTCATTTGTTGTAAGTAGGGTTAATCGAGTATCAGGTTCACAGTATCCTGCCC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCTGCAACTCATTTGTTGTAAGTAGGGTTAATCGAGTATCAGGTTCACAGTATCCTGCCC  480
```

```
Query  481  TTATTATTTTATGATTCACTGACTCAAGTTCCA  513
            |||||||||||||||||||||||||||||||||
Sbjct  481  TTATTATTTTATGATTCACTGACTCAAGTTCCA  513
```

## Sequence 947 matched with Sequence 379

Query= Sequence ID 947
Length=646


   SEQ ID NO: 379

ALIGNMENTS
 Identities = 646/646 (100%), Gaps = 0/646 (0%)

```
Query  1    GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAGAGTGAAAAAATTCTGGTACAAATTGGGAAATTAGTATATAACAACATAGTGTTAAAT  60

Query  61   TCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGATAAAAATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGATAAAAATG  120

Query  121  GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GACCGTCCTATCACATACAAAATTGTTTTTTAGATAAAGATTTAAATACAGGCACTCCTT  180

Query  181  CATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGCTGAAACTGCAAAGCAA  240

Query  241  TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCCTGTGACCGTTAAAATTTTCATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCCTGTGACCGTTAAAATTTTCATT  300

Query  301  AAACTATTAAAAACACCCATGACTGGTCACaaatgtattgggaaatggaaaagaattaat  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAACTATTAAAAACACCCATGACTGGTCACAAATGTATTGGGAAATGGAAAAGAATTAAT  360

Query  361  acactaaaaatacaaaaaatagaaaatatttaaaattatctaaaaatttgaaacattaga  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACACTAAAAATACAAAAAATAGAAAATATTTAAAATTATCTAAAAATTTGAAACATTAGA  420

Query  421  aaaattGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAATTGAGAACTAGGCAGGGCGTGGTGGCTCACATCTGTAATTTTAGCCCTTTGGGAGG  480
```

```
Query  481  CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTGANGCAGGTGGATCACCTGANGTCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAA  540

Query  541  CCCCGTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CCCCGTCTCTACTGAAAATACAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCT  600

Query  601  TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCANGANG  646
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGCTNACCAGGANGCTGAGGCAGGAGAATCACTTGAACCCANGANG  646
```

Blast comparison trimmed "NGANG" from the 3' end of both sequences and reported 641 identities. The report has been manually corrected for this. "NGANG" has been appended to both sequences and identity count has been increased to 646.

# Sequence 949 matched with Sequence 380

Query=   Sequence ID 949
Length=362


    SEQ ID NO: 380

ALIGNMENTS
 Identities = 362/362 (100%), Gaps = 0/362 (0%)

```
Query  1    GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTAATGT   60

Query  61   TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TACCACTAAGGCCCTGCCCCAGCTTTATCACCTGAGCACTAACAAGTGCTGTGTGGAGTT   120

Query  121  CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAACAATTACCACCGTGGAG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAACAATTACCACCGTGGAG   180

Query  181  GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTAATTAGNGAAAGAGGGA   240

Query  241  TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCCAGNGGTAAGCAATAATTG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCCCCAGNGGTAAGCAATAATTG   300

Query  301  TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TANAGACTGGATTTNANAAGCCCTGAGAGTTTATTTTCAACCTATNTATTATAGNNCAAT   360

Query  361  CC   362
            ||
Sbjct  361  CC   362
```

# Sequence 1028 matched with Sequence 381

Query=   Sequence ID 1028
Length=80


   SEQ ID NO: 381

ALIGNMENTS
 Identities = 80/80 (100%), Gaps = 0/80 (0%)

```
Query  1    ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAGATGG  60

Query  61   GGTCAAGGCACCAGGACTGA  80
            ||||||||||||||||||||
Sbjct  61   GGTCAAGGCACCAGGACTGA  80
```

# Sequence 1056 matched with Sequence 382

```
Query=   Sequence ID - 1056                  nt:     435
Length=435


   SEQ ID NO: 382               nt:     435

ALIGNMENTS
 Identities = 435/435 (100%), Gaps = 0/435 (0%)

Query  1    TCGCTTGTAAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCGCTTGTAAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTCACAC  60

Query  61   CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGT  120

Query  121  CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCG  180

Query  181  TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCCGATCATCTTTCCTGTTCCAGAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCCGATCATCTTTCCTGTTCCAGAGA  240

Query  241  AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTT  300

Query  301  ACTTCCCTAATGAAGTTAAGAACCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACTTCCCTAATGAAGTTAAGAACCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGA  360

Query  361  AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGGGTTGATGGATTAATTAAATAAGTCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACC  420

Query  421  TGAGAACCTTCCAGA    435
            |||||||||||||||
Sbjct  421  TGAGAACCTTCCAGA    435
```

# Sequence 1071 matched with Sequence 383

Query=   Sequence ID 1071
Length=571


   SEQ ID NO: 383

ALIGNMENTS
 Identities = 571/571 (100%), Gaps = 0/571 (0%)

```
Query  1    NGATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    NGATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAGGACTA  61

Query  62   ACCCCCCTGCCTTCTGCATAATGAATTAACTAGAAATAACTTNGCAAGGAGAGCCAAAGC   121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   ACCCCCCTGCCTTCTGCATAATGAATTAACTAGAAATAACTTNGCAAGGAGAGCCAAAGC   121

Query  122  TAAGACCCCNGAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG   181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  TAAGACCCCNGAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGCACACCCGTCTATG   181

Query  182  TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG   241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  TAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAG   241

Query  242  CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCCACAGAACCCTCTAAAT   301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242  CTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTNGCCCACAGAACCCTCTAAAT   301

Query  302  CCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302  CCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAA  361

Query  362  CCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  362  CCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTA  421

Query  422  AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  422  AGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCC  481
```

```
Query  482   TNACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGTATAAGTAACA   541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  482   TNACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGTATAAGTAACA   541

Query  542   TGAAAACATTCTCCTCCGCATAAGCCTGC   571
             |||||||||||||||||||||||||||||
Sbjct  542   TGAAAACATTCTCCTCCGCATAAGCCTGC   571
```

Blast comparison trimmed "N" from both the 3' end and the 5' end of both sequences and reported 569 identities. The report has been manually corrected for this. "N" has been appended to both sequences and prepended to both sequences and identity count has been increased to 571.

# Sequence 1074 matched with Sequence 384

```
Query=   Sequence ID - 1074                    nt:      689
Length=689


   SEQ ID NO: 384                 nt:      689

ALIGNMENTS
 Identities = 689/689 (100%), Gaps = 0/689 (0%)

Query  1     GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAACAAA   60

Query  61    GCGAAACTCTGTCTCaaaaaaaaaaaaaaaaaaaaTTTGTTGACTGTTGTAATTTAAAGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGAAACTCTGTCTCAAAAAAAAAAAAAAAAAAAATTTGTTGACTGTTGTAATTTAAAGC   120

Query  121   TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGATGAACCAGGTTC   180

Query  181   TGCACAAAGTACCTTATGTTCATGGCCTCATATCGTCTTCTCCAAAACTCTGCAAGATAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGCACAAAGTACCTTATGTTCATGGCCTCATATCGTCTTCTCCAAAACTCTGCAAGATAG   240

Query  241   GATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAAATTGTACCCAAGGTCACACA   300

Query  301   GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTCANAGTGCCTCTCCTGCCGTAGG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGTTCANAGTGCCTCTCCTGCCGTAGG   360

Query  361   CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CTTATCACAAAAAGTCAAAGTTTGGTCATAATAAAGCCTGAAGTTTGGCAGGATTTAAAA   420

Query  421   ATAGTCACCANACTTTTGAGTTGGAGCATCCCACCTCACTGCTGTTCACCTTCTGTGGCA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   ATAGTCACCANACTTTTGAGTTGGAGCATCCCACCTCACTGCTGTTCACCTTCTGTGGCA   480
```

```
Query  481  GGGAGAGTCATCATTTCCATTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGAGAGTCATCATTTCCATTTCAGCTTGTGGAATATCTTGTCATTAACATTCTCATGCA  540

Query  541  AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAGCCATTTTATGGTGCCCAATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGC  600

Query  601  CTTCCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CTTCCTAATTTTGGACTTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAA  660

Query  661  ATATTTTCTTCACTTTTCATTCATTCTAC  689
            |||||||||||||||||||||||||||||
Sbjct  661  ATATTTTCTTCACTTTTCATTCATTCTAC  689
```

# Sequence 1081 matched with Sequence 385

Query=  Sequence ID 1081
Length=542


   SEQ ID NO: 385

ALIGNMENTS
 Identities = 542/542 (100%), Gaps = 0/542 (0%)

```
Query   1    cgccgccgcgccgccgtcgctctccaacgccagcgccgcctctcgctcgccgagctccag  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCTCCAG  60

Query   61   ccgAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAAAGCAGACT  120

Query   121  GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCTCGC  180

Query   181  AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTACAGGCCTGGTACTGTG  240

Query   241  GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGCAAACTTCCC  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAACTTCTGATTCGCAAACTTCCC  300

Query   301  TTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTTAAAACAGATCTGCGCTTCCAGAGC  360

Query   361  GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GCANCTATCGGTGCTTTGCAGGAGGCAAGTGAGGCCTATCTGGTTGGCCTTTTTGAAGAC  420

Query   421  ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  ACCAACCTGTGTGCTATCCATGCCAAACGTGTAACAATTATGCCAAAAGACATCCAGCTA  480
```

```
Query  481  GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCATTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCACGCCGCATACGTGGAGAACGTGCTTAAGAATCCACTATGATGGGAAACATTTCATTC  540

Query  541  TC  542
            ||
Sbjct  541  TC  542
```

# Sequence 1083 matched with Sequence 386

Query=  Sequence ID - 1083                      nt:     198
Length=198


   SEQ ID NO: 386                  nt:     198


ALIGNMENTS
 Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query  1    GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG  60

Query  61   TTGTACTCTGNNGACAGCCTTCTTTaaaaaaaaaaataaacaatttaaaacaaaaaaaaa  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAAATAAACAATTTAAAACAAAAAAAAA  120

Query  121  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  180

Query  181  aaaaaaaaanTTTTAACC  198
            ||||||||||||||||||
Sbjct  181  AAAAAAAAANTTTTAACC  198

# Sequence 1084 matched with Sequence 387

```
Query=   Sequence ID - 1084                    nt:     198
Length=198


   SEQ ID NO: 387                  nt:      198

ALIGNMENTS
 Identities = 198/198 (100%), Gaps = 0/198 (0%)

Query  1     GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACATTGG   60

Query  61    TTGTACTCTGNNGACAGCCTTCTTTaaaaaaaaaaataaacaatttaaaacaaaaaaaaa   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAAACAATTTAAAACAAAAAAAAAA   120

Query  121   aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   180

Query  181   aaaaaaaaanTTTTAACC   198
             ||||||||||||||||||
Sbjct  181   AAAAAAAAANTTTTAACC   198
```

# Sequence 1099 matched with Sequence 388

Query=  Sequence ID - 1099                    nt:     561
Length=561


   SEQ ID NO: 388                nt:     561

ALIGNMENTS
 Identities = 561/561 (100%), Gaps = 0/561 (0%)

```
Query   1    TGCATGCTTGTGGATTGGAAAAACTTTGGAGACTGATTACTTTTCATTATATATGTGTCA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TGCATGCTTGTGGATTGGAAAAACTTTGGAGACTGATTACTTTTCATTATATATGTGTCA   60

Query   61   CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CAGTGAAACAGCTTTTATGTGTCATGTAAGATTACTGCTTGCCTCTCTAAGGAAGGTCGT   120

Query   121  GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GACTGTTTAAATAGACGGGCAAGGTGGAACCTTTTGAAAGATGAGCTTTTGAATATAAGT   180

Query   181  TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAGATCTGCTGACTTATAT   240

Query   241  AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAATGTTCAATGTTGAAATTTCT   300

Query   301  GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGAGAGTGAGGAAGCATTCTTTCCTTC   360

Query   361  ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ACTAAGTTTGTCTTTCTTGTCTTCTGGATAGATTGATTTTAAGAGACTAAGGGAATTTAC   420

Query   421  AAACTAAAGATTTTAGTCATCTGGTGGAAAAGGAGACTTTAAGATTGTTTAGGGCTGGGC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AAACTAAAGATTTTAGTCATCTGGTGGAAAAGGAGACTTTAAGATTGTTTAGGGCTGGGC   480
```

```
Query  481   GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GGGGTGACTCACATCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGA   540

Query  541   AGGAGTTCAAGACCAGCGTGG   561
             |||||||||||||||||||||
Sbjct  541   AGGAGTTCAAGACCAGCGTGG   561
```

# Sequence 1109 matched with Sequence 389

Length=601
 Identities = 601/601 (100%), Gaps = 0/601 (0%)

```
Query  1    TTTGNCGGTNTTGGannnnnnanaanTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTGNCGGTNTTGGANNNNNNANAANTTTCTTCCANNCNTNACNTNTTGGTGGNCTAAATT  60

Query  61   AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATTNTCNTNCN  120

Query  121  NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  NNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCNTNAATTANCATC  180

Query  181  CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATANCNANNATAANANCTCC  240

Query  241  TGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNCCCNCAGAGTNAACTCATCCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNCCCNCAGAGTNAACTCATCCT  300

Query  301  CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTaannanaccngtan  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGCGCGANATATTAANNANACCNGTAN  360

Query  361  ntnnnanacannanntnngnaanaanccttctnannTTTTAGCNTCNNGCNNTAACNNNN  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  NTNNNANACANNANNTNNGNAANAANCCTTCTNANNTTTTAGCNTCNNGCNNTAACNNNN  420

Query  421  NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  NTCTTNGTGNNNNCNCAGCTTTCNCNNCATNATNCTNCNNCGAANTNTCANNCNTCTCCN  480

Query  481  CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTTNAATGNNTTCCCATGNATTAANTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNAT  540

Query  541  TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGTNNNNCNN  601
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATNGNCNNTTTACNTCATGTGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGTNNNNCNN  601
```

Blast comparison trimmed "NNNNCNN" from the 3' end of both sequences and reported 594 identities. The report has been manually corrected for this. "NNNNCNN" has been appended to both sequences and identity count has been increased to 601.

# Sequence 1118 matched with Sequence 390

Query=   Sequence ID 1118
Length=616


   SEQ ID NO: 390

ALIGNMENTS
 Identities = 616/616 (100%), Gaps = 0/616 (0%)

```
Query   1    GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCCACGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCCACGG   60

Query   61   TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTCGGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGGGGTTCGGC   120

Query   121  CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACATTAAGCAGTACAG   180

Query   181  CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGAAGCTGTTCCAAAGTTT   240

Query   241  GAAGAGATGTTTGCTAGTAGATTCACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GAAGAGATGTTTGCTAGTAGATTCACAGAAAATGACAAGGAGTATCAGGAATACCTGAAA   300

Query   301  CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  CGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGGAATAGCANAGCTGGTGGGAACCAA   360

Query   361  AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  AGAAACAGAGGCAATCGGTTGCAAGACAACAGACAGTTCAGAGGCAGGGACAACAGATGG   420

Query   421  GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACTAC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GGGTGGCCAAGTGACAATCGATCCAATCAGTGGCATGGACGATCCTGGGGTAACAACTAC   480
```

```
Query   481   CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   CCGCAACACAGACAAGAACCTTACTATCCCCAGCAATATGGACATTATGGTTACAACCAG   540

Query   541   CGGCCTCCTTACGGTTACTACTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACT   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   CGGCCTCCTTACGGTTACTACTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACT   600

Query   601   CTGTTACCATGAGAAA   616
              ||||||||||||||||
Sbjct   601   CTGTTACCATGAGAAA   616
```

# Sequence 1125 matched with Sequence 391

Query=   Sequence ID 1125
Length=407


   SEQ ID NO: 391

ALIGNMENTS
 Identities = 407/407 (100%), Gaps = 0/407 (0%)

```
Query  1    NGACTGGCTCCCGAAAAGAAGGGTGGCGAGaanaaaaaGGGCCGTTCTGCCATGGACGAAG  61
            |||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||||||
Sbjct  1    NGACTGGCTCCCGAAAAGAAGGGTGGCGAGAANAAAAAGGGCCGTTCTGCCATGGACGAAG  61

Query  62   TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA   121
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  62   TGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGGGCTTCAAGA   121

Query  122  ANCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTC  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  ANCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAGGAGATGGGAACTC  181

Query  182  CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG  241
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  182  CATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGCCAAAGGAATAAGGAATG  241

Query  242  TGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTAATGAGGATGAAGATTCACCAA  301
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  242  TGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTAATGAGGATGAAGATTCACCAA  301

Query  302  ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG  361
            ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302  ATAAGCTNTATACTTTGGTTACCTATGTACCTGTTACCACTTTCAAAAATCTACAGACAG  361

Query  362  TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCaaanaaaNT    407
            ||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  362  TCAATGTGGATGANAACNAATCGCTGATCGTCAGATCAAANAAANT    407
```


Blast comparison trimmed "N" from the 5' end of both sequences and trimmed "NT" from
the 3' end of both sequences and reported 404 identities. The report has been manually

corrected for this. "N" has been prepended to the 5' end of both sequences and "NT" has appended to the 3' end of both sequencies and identity count has been increased to 407.

# Sequence 1139 matched with Sequence 392

```
Query=   Sequence ID - 1139                    nt:      503
Length=503


   SEQ ID NO: 392                  nt:      503

ALIGNMENTS
 Identities = 503/503 (100%), Gaps = 0/503 (0%)

Query  1    CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTGTGGA  60

Query  61   CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTCAGCGCATGCACCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTCAGCGCATGCACCT  120

Query  121  TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAAGCCTTAAGCACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAAGCCTTAAGCACA  180

Query  181  ATTAATTAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTAATTAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCCACCATAGGGCATGATT  240

Query  241  AACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAAACCCCCTTTTCCCTTCAGCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAAACCCCCTTTTCCCTTCAGCT  300

Query  301  TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGaaaaaggaaaaaaggcc  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGGCCTACAGAAAAAGGAAAAAAGGCC  360

Query  361  acaaaagttccctctcactttcagtaaaaataaataaaacagcagcagcaaacaaataaa  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACAAAAGTTCCCTCTCACTTTCAGTAAAAATAAATAAAACAGCAGCAGCAAACAAATAAA  420

Query  421  atgaaataaaagaaacaaatgaaataaatattgtgttgtgcagcattaaaaaaaatcaaa  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATGAAATAAAAGAAACAAATGAAATAAATATTGTGTTGTGCAGCATTAAAAAAAATCAAA  480
```

```
Query  481  ataaaaattaaatGTGAGCAAAG  503
            |||||||||||||||||||||||
Sbjct  481  ATAAAAATTAAATGTGAGCAAAG  503
```

# Sequence 1148 matched with Sequence 393

Query=   Sequence ID - 1148                    nt:      587
Length=587


    SEQ ID NO: 393                 nt:      587

ALIGNMENTS
 Identities = 587/587 (100%), Gaps = 0/587 (0%)

Query  1     TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAAAACG  60

Query  61    CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTTGTGGTGTG  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTTGTGGTGTG  120

Query  121   GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCTGACATTTGAAAA  180

Query  181   TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTTAAGAAAACCAATAAAATCATTAA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TACGCAGTTTGCATTTGATACGTCAAATGTTATTTTTAAGAAAACCAATAAAATCATTAA  240

Query  241   AACCGAAAAGGCAGTTTTGCTTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACCGAAAAGGCAGTTTTGCTTGTTTTTACCTTAGTTGGAGTTATCTGCAATTGCCGTAT  300

Query  301   TAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGTCCCCTTTAGAGCTACGAAACATGT  360

Query  361   CAATTTTACTTTTCTCCAGCTTTTTGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CAATTTTACTTTTCTCCAGCTTTTTGGAATCTTATCTAAATTACCATGTAGAGTTCTGCA  420

Query  421   TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTCACCGTT  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAGCTTCAAATTCTCTTAGCCAATGTGGTCTGTAAGTGTCTATCGATGAATTTCACCGTT  480

```
Query  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AATTGCCGTAGTATACTGTCCTGTACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCAC  540

Query  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGTTGCTCCCATGGTAGGAANGAATGGCTTATCAATGGTCGGATTT  587
```

# Sequence 1160 matched with Sequence 394

```
Query=   Sequence ID - 1160                    nt:      650
Length=650


   SEQ ID NO: 394                  nt:     650

ALIGNMENTS
 Identities = 650/650 (100%), Gaps = 0/650 (0%)

Query  1     GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGTACAG   60

Query  61    CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAACCAAACAA   120

Query  121   CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAAGAAACTAT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTGTAAAGAAACTAT   180

Query  181   AGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAGCAGAAGGATATGAACC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAGCAGAAGGATATGAACC   240

Query  241   TTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACAGCTTGTGATGTCCTTCTTCG   300

Query  301   CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTTAACACGAAGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CTTTACTCCAATCCCTATTATAGACAGATTTAGTGATTCCTGGTCTTTTTAACACGAAGA   360

Query  361   ATATCTATTGTTTTCTCTTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATATCTATTGTTTTCTCTTTTGTAGGATCTGTATGATTTTATCTACTTAACAGATAGCAC   420

Query  421   TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTCATAATTTCTGATTGGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAATTAGATTAAAATTCTATAAGAAACTTTTTAATTTGCTGTTCATAATTTCTGATTGGT   480
```

```
Query  481  ATGCAATAACTGTTTCAATGAAAATCAATGTAATTTAGTATTTTAATATTTGCACCTTTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATGCAATAACTGTTTCAATGAAAATCAATGTAATTTAGTATTTTAATATTTGCACCTTTG  540

Query  541  TGAAATATAGTAAATAAATTAAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGAAATATAGTAAATAAATTAAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCAC  600

Query  601  AATCCTGGGTTGGGAGCCAGTGGATTTCCTGAAACACAGATTTGTTAATG  650
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AATCCTGGGTTGGGAGCCAGTGGATTTCCTGAAACACAGATTTGTTAATG  650
```

# Sequence 1165 matched with Sequence 395

```
Query=   Sequence ID - 1165                    nt:     502
Length=502


   SEQ ID NO: 395                 nt:     502


ALIGNMENTS
 Identities = 502/502 (100%), Gaps = 0/502 (0%)

Query  1    CTCAAGTGAATCCTGGCTTCTTGGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCAAGTGAATCCTGGCTTCTTGGAAGCGCTTGCCTAGACGAGACACAGTGCATAAAAAC  60

Query  61   AACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGGCAAGACAA  120

Query  121  GCAGTGTGGCCAGAATTTTGAACTTCTGATGAATGTGTAATGCAAAGGACCTTGTACAtt  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCAGTGTGGCCAGAATTTTGAACTTCTGATGAATGTGTAATGCAAAGGACCTTGTACATT  180

Query  181  tttttGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTTTGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCTGTGAAACTTTAAGTGG  240

Query  241  CCCTACTGCGCAGAAGCATTCAGATGTCACTTGATGATCTGTAAGGGAACTTGCTGATTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCCTACTGCGCAGAAGCATTCAGATGTCACTTGATGATCTGTAAGGGAACTTGCTGATTT  300

Query  301  GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGGAATGTGCTTAGGGAACACACATTCCTTTTGACAGGGTCTGTCACTGGGTGGGTGATG  360

Query  361  AATTATACAGATGACATGTGCttttttttctttttttCAACCTCAATGGTATTCCTACAGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATTATACAGATGACATGTGCTTTTTTTTCTTTTTTCAACCTCAATGGTATTCCTACAGG  420

Query  421  AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGGAATACAATTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAATGGATAACCATTTTAACTGTATTTTTTGCAGCCCGTACCTTCTTGGGAATACAATTG  480
```

```
Query  481  TCTAACTTTTTATTTTTGGTCT  502
            ||||||||||||||||||||||
Sbjct  481  TCTAACTTTTTATTTTTGGTCT  502
```

# Sequence 1172 matched with Sequence 396

Query=  Sequence ID - 1172                   nt:     648
Length=648


   SEQ ID NO: 396                  nt:    648

ALIGNMENTS
 Identities = 648/648 (100%), Gaps = 0/648 (0%)

Query  1     CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACAAATA  60

Query  61    ACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAATGGATTCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAATGGATTCC  120

Query  121   ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTCACCCAGTTATAT  180

Query  181   GCTGCCTACAACAAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GCTGCCTACAACAAACTCACTTCACCTGTAAACATACATATGGATGGAAAGAGAAGGCAT  240

Query  241   GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAACAAAGGTGGCTATTCTTATAT  300

Query  301   GAGATAATACAGACATTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAGATAATACAGACATTAAATCAAAAACTGGAAACAAACACAAAGTCATTGTATAATGAT  360

Query  361   GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GAATTCAATTATATCATGATGAATTCAATTATATCCTCCTTCCTGATCAATTCAGAAAGG  420

Query  421   AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AGGATATAATCTTTTTAAATATATATACACCCAACACCAGAGCATATAAATATGTAAAGG  480

```
Query   481   AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAATATTTTATCTAAA   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AAGATAAAGGGAGTCCTGTGATCAAGAATAAATATAACAATTATAAATATTTTATCTAAA   540

Query   541   GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   GTGATAGATAGACTGTAATACAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTG   600

Query   601   GACTGATCATCTAGAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT   648
              ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   GACTGATCATCTAGAAGGGAGAAAAAGCTTTATGATTGGAAAAGCCAT   648
```

# Sequence 1178 matched with Sequence 397

Query=   Sequence ID 1178
Length=705


   SEQ ID NO: 397

ALIGNMENTS
 Identities = 705/705 (100%), Gaps = 0/705 (0%)

```
Query  1    ATTGTGTTGGCCACCCGGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATTGTGTTGGCCACCCGGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACATGCCT   60

Query  61   CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACAAGAAGAAA   120

Query  121  CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCAGGTGAGGAGACG   180

Query  181  GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAATGTTGTAGTGTTAGCT   240

Query  241  GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTTCGCCTGTGGAAAATATTTTC   300

Query  301  CCTGATACTCTTAAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTGATACTCTTAAAATTTGAATGTATGAGACTGGCAAAGTTTTGCATCTTAGGAGGAGT   360

Query  361  GATTCATTTCACCGTGATCTCTCATCACATTTCACATACAACCCCTACGtttttttGTGT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATTCATTTCACCGTGATCTCTCATCACATTTCACATACAACCCCTACGTTTTTTTGTGT   420

Query  421  TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGGAAACAATGTAATGGATGATGAGTTGGGCATAAGTGCAGGAAAGACGGGTGTAATAG   480
```

```
Query   481   AGGaaaaaaaTGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AGGAAAAAAATGTTATCTGCTTTTCTTTCAGGATGCTATAAAATCACCACGGTCTTTAGC   540

Query   541   CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   CATGCACAAACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGA   600

Query   601   GGAAAAGCAAGGCTTACAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCT   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   GGAAAAGCAAGGCTTACAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCT   660

Query   661   GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT   705
              |||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   GAGTCAANATGAGTGGGAAACCATCTCAATAAACACATTTTGGAT   705
```

# Sequence 1180 matched with Sequence 398

Query=  Sequence ID - 1180                     nt:      622
Length=622


    SEQ ID NO: 398                nt:     622


ALIGNMENTS
 Identities = 622/622 (100%), Gaps = 0/622 (0%)

Query   1     CTTTTCCTCCCGCTGTCCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGT   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1     CTTTTCCTCCCGCTGTCCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGT   60

Query   61    GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC   120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61    GAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTC   120

Query   121   GGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT   180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121   GGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACT   180

Query   181   AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGT   240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181   AACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGT   240

Query   241   CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241   CAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGG   300

Query   301   AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301   AAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACT   360

Query   361   ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTG   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361   ATTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTG   420

Query   421   GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT   480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421   GGTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGAT   480

```
Query  481   GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GCTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGA   540

Query  541   AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACANCCA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACANCCA   600

Query  601   CAATCATGAGGATGATGTGTTG   622
             ||||||||||||||||||||||
Sbjct  601   CAATCATGAGGATGATGTGTTG   622
```

# Sequence 1181 matched with Sequence 399

Query=   Sequence ID - 1181                    nt:     155
Length=155


   SEQ ID NO: 399                nt:     155

ALIGNMENTS
 Identities = 155/155 (100%), Gaps = 0/155 (0%)

Query  1     CGCCACTTATCCAGTGAACCACTATCACGaaaaaaaCTCTACCTCTCTATACTAATCTCC  60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATACTAATCTCC  60

Query  61    CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTaaaaaaaaaa  120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAAAAAAAAAA  120

Query  121   aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa   155
             |||||||||||||||||||||||||||||||||||
Sbjct  121   AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   155

# Sequence 1182 matched with Sequence 400

```
Query=   Sequence ID 1182
Length=700


   SEQ ID NO: 400

ALIGNMENTS
 Identities = 700/700 (100%), Gaps = 0/700 (0%)

Query  1    CATTGTGTTGGCNCCCGGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAGCAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CATTGTGTTGGCNCCCGGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAGCAGA  60

Query  61   AATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTCTCCTTTGA  120

Query  121  TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAAGGAAGCTGGGAT  180

Query  181  CAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAGGAATTCAGGCTGGAAA  240

Query  241  GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACGTTACTCTTCTCCTTCGCCCA  300

Query  301  GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCCATTTGTTGGGCGCATCCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCATCTCCCCATTTGTTGGGCGCATCCT  360

Query  361  TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGATTGGCATGTGGCAAACACCGACAAGAAATCCTATGAGCCCCTGGAAGACCCTGGGGT  420

Query  421  AAAGAGTGTCACTAAAATCTACAACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAGAGTGTCACTAAAATCTACAACTACTACAAGAAGTTTAGCTACAAAACCATTGTCAT  480
```

```
Query  481  GGGCGCCTCCTTCCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGCGCCTCCTTCCGCAACACGGGCGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCAC  540

Query  541  CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CATCTCACCCAAGCTCCTGGGAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCT  600

Query  601  CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CTCAGCCAAGGCGGCCCAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTT  660

Query  661  CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG  700
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CCGTTGGTTGCACAACGAGGACCAGATGGCTGTGGAGAAG  700
```

# Sequence 1183 matched with Sequence 401

```
Query=   Sequence ID - 1183                nt:      479
Length=479


   SEQ ID NO: 401              nt:      479

ALIGNMENTS
 Identities = 479/479 (100%), Gaps = 0/479 (0%)

Query  1     CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CGTGGCAGCCATCTCCTTCTCGGCATCATGGCCGCCCTCAGACCCCTTGTGAAGCCCAAG   60

Query  61    ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    ATCGTCAAAAAGAGAACCAAGAAGTTCATCCGGCACCAGTCAGACCGATATGTCAAAATT   120

Query  121   AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AAGCGTAACTGGCGGAAACCCAGAGGCATTGACAACAGGGTTCGTAGAAGATTCAAGGGC   180

Query  181   CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACaaaaaaaCAAAGCACATGCTGCCC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAAACAAAGCACATGCTGCCC   240

Query  241   AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AGTGGCTTCCGGAAGTTCCTGGTCCACAACGTCAAGGAGCTGGAAGTGCTGCTGATGTGC   300

Query  301   AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AACAAATCTTACTGTGCCGAGATCGCTCACAATGTTTCCTCCAAGAACCGCAAAGCCATC   360

Query  361   GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTGGAAAGAGCTGCCCAACTGGCCATCAGAGTCACCAACCCCAATGCCAGGCTGCGCAGT   420

Query  421   GAAGAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAAACTG   479
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GAAGAAAATGAGTAGGCAGCTCATGTGCACGTTTTCTGTTTAAATAAATGTAAAAACTG   479
```

# Sequence 1185 matched with Sequence 402

Query=   Sequence ID - 1185                    nt:      628
Length=628


   SEQ ID NO: 402                  nt:      628

ALIGNMENTS
 Identities = 628/628 (100%), Gaps = 0/628 (0%)

```
Query  1    CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTTGATTACCTTTGAGTATTAGGTTGAAAGCTTCTCTGTGCTTGATTGAACATTGTGAT  60

Query  61   GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAATGTTTAATGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GATGTTGATTGGGTCATGTCAGATTTAGACAGTGTTGTGTTTAAGATAAATGTTTAATGG  120

Query  121  CTCTTAGCAGTGTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTCTTAGCAGTGTTCATGCCTCCCCTTTTCCCCTGATACTTTAAAAACAGAATATACAGA  180

Query  181  AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGTCTACCAGCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAGTAGTGTCTACCAGCTG  240

Query  241  TTTTCACATTTTTCTGTTTCCTTCTGTCCTTGGAATCCtttttttAGATCCTTGTAATAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTTCACATTTTTCTGTTTCCTTCTGTCCTTGGAATCCTTTTTTTAGATCCTTGTAATAC  300

Query  301  TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTTTCCATTTTGCTCCATGGTCTTCAT  360

Query  361  AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AATGCCCTGTGGTCCTTTATTAAGGGGATGCACCATGTAGAGGTGAAAGGCTTTCCTTGA  420

Query  421  CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTGGCCACCATTTCTGTATTTTCCTTAGAGGAGGAGGTTTCCAACATTTCTTTTTTAGA  480
```

```
Query  481  GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GACAGAGTCTCGTTCTGACACGCAGGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCA  540

Query  541  GCCTCGAACTCCTGGGCTCAAGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCCTCGAACTCCTGGGCTCAAGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTG  600

Query  601  CAGGTGCCTGCCACCACACCCAGCTAAT  628
            ||||||||||||||||||||||||||||
Sbjct  601  CAGGTGCCTGCCACCACACCCAGCTAAT  628
```

# Sequence 1186 matched with Sequence 403

Query= Sequence ID - 1186                    nt:     494
Length=494


    SEQ ID NO: 403                  nt:     494

ALIGNMENTS
 Identities = 494/494 (100%), Gaps = 0/494 (0%)

Query  1    CAGCCCTCCGTCACCTCTTCACCGCACCCTCGGACTgccccaaggcccccgccgccgcct  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGCCCTCCGTCACCTCTTCACCGCACCCTCGGACTGCCCCAAGGCCCCCGCCGCCGCCT  60

Query  61   ccagcgccgcgcagccaccgccgccgccgccgcctctccttagtcgccgccATGACGACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCAGCGCCGCGCAGCCACCGCCGCCGCCGCCGCCTCTCCTTAGTCGCCGCCATGACGACC  120

Query  121  GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCGTCCACCTCGCAGGTGCGCCAGAACTACCACCAGGACTCAGAGGCCGCCATCAACCGC  180

Query  181  CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCATGTCTTACTACTTTGAC  240

Query  241  CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAG  300

Query  301  AGGGGAACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGGGGAACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGGTGGCCGAATCTTCC  360

Query  361  TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCAGGATATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGT  420

Query  421  GTGCATTACATTTGGaaaaaaaTGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGCATTACATTTGGAAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA  480

```
Query  481  CTGACAAAATGAC  494
            |||||||||||||
Sbjct  481  CTGACAAAATGAC  494
```

# Sequence 1188 matched with Sequence 404

```
Query=   Sequence ID - 1188                nt:     599
Length=599


   SEQ ID NO: 404              nt:     599


ALIGNMENTS
 Identities = 599/599 (100%), Gaps = 0/599 (0%)

Query  1     GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCCTGTGCAACAGCCACTACAT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCCTGTGCAACAGCCACTACAT   60

Query  61    TACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAG   120

Query  121   TCTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAG   180

Query  181   ATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAAATCTACAGTACACCA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAAATCTACAGTACACCA   240

Query  241   CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCANA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCANA   300

Query  301   GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAA   360

Query  361   CCTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAG   420

Query  421   GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGC   480
```

Page 677

```
Query  481  TCTTTCCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCTTTCCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCT  540

Query  541  TGAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG  599
```

# Sequence 1189 matched with Sequence 405

```
Query=   Sequence ID 1189
Length=610


   SEQ ID NO: 405

ALIGNMENTS
 Identities = 610/610 (100%), Gaps = 0/610 (0%)

Query  1    GGGAGACAAGCCCAGCCTTTCGGCGAGATACGTCTAACCCTGTGCAACAGCCACTACATT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGGAGACAAGCCCAGCCTTTCGGCGAGATACGTCTAACCCTGTGCAACAGCCACTACATT  60

Query  61   ACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTTTTTCCAGT  120

Query  121  CTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTTAGTGGGGGCGGGGTGGGAAAGA  180

Query  181  TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAAATCTACAGTACACCAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAAATCTACAGTACACCAC  240

Query  241  AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCAGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCGTGGAAAGGGGCAGGCCAGAG  300

Query  301  CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATGCCATCTCAAC  360

Query  361  CTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCTTCCCCGCCCGTTTTACAAAGGGGGAGGCTAAAGCCCAGAGACAGCTTGATCAAAGG  420

Query  421  CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCAGCTCAGGGCT  480
```

```
Query  481  CTTTCCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTTTCCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCCTGTCTCAGGGTGAGGTGCTT  540

Query  541  GAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAGCC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAGTCTCCAACGGCAAGGGAACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAGCC  600

Query  601  TCGAGGAGGT  610
            ||||||||||
Sbjct  601  TCGAGGAGGT  610
```

# Sequence 1190 matched with Sequence 406

Query=   Sequence ID 1190
Length=644


   SEQ ID NO: 406

ALIGNMENTS
 Identities = 644/644 (100%), Gaps = 0/644 (0%)

```
Query  1    GTTTAAATTTGACAAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTTAAATTTGACAAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATTTTCC  60

Query  61   ATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTAtttttttGCAGTAAGTTATAATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTATATTTTTTGCAGTAAGTTATAATG  120

Query  121  ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAACTATAATTATCAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAACTATAATTATCAG  180

Query  181  TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAAACTAGGCTATATATACATTGGGAAAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAAAGTCCTGTGGTATTTTTCAATTTGTAAGAAACTAGGCTATATATACATTGGGAAAAA  240

Query  241  CAGCCTTCATTTGTCAATGCACTAGTGTTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAGCCTTCATTTGTCAATGCACTAGTGTTCCAAAGGTTTCTGGTAATTGTGTGCTATTGC  300

Query  301  TTTTTGTTGACTTGCaaaaaaaaaaaaaaaaaaaaTTACTATGACTTGNGGTAGCCCTGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTTGTTGACTTGCAAAAAAAAAAAAAAAAAAAATTACTATGACTTGNGGTAGCCCTGCA  360

Query  361  ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACCTTCGGAAGTGCTTAGCCCAGTCTGACCATACATTTATATTTANAATGCTTAGGTAAA  420

Query  421  TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAATAATATGCCTAAACCCAATGCTATAAGATACTATATAATATCTCATAATTTTAAAA  480
```

```
Query  481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCACTGTTTTGTATAATAATAAAACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGT  540

Query  541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAGGGTGCTGAGGAAGAAAAACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAA  600

Query  601  TGTCCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGTCCTAATCAATGAAGCTGTGTGATGATTCTGATTGACAGAGA  644
```

# Sequence 1191 matched with Sequence 407

Query=  Sequence ID 1191
Length=653


   SEQ ID NO: 407

ALIGNMENTS
 Identities = 653/653 (100%), Gaps = 0/653 (0%)

```
Query  1    GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAATGTTA  60

Query  61   ATTTTGGATCACACACATTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTTTGGATCACACACATTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGAGTAGCTAT  120

Query  121  ATTATTTCTAGTTAAAAAACTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTATTTCTAGTTAAAAAACTCTCTATATACATATTTATTTGTTTTTCTACTTGTTTAAT  180

Query  181  ATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATATTTAAATGTATTTTACT  240

Query  241  CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGgagagtgagagcaagagtaagag  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGGAGAGTGAGAGCAAGAGTAAGAG  300

Query  301  agagagCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGAGAGAGCACGCATAGATGGAAGCACACATTTAATGTCTATGAAATGAGAAAACATTAA  360

Query  361  GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGCTAAGATATTTTTCCTTCTGAACTAGCAGATTGTATCAATGGCTGGTCACTTAAATTA  420

Query  421  ATCAGTTTGTAAAGATATTTAAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATCAGTTTGTAAAGATATTTAAAAGGTATGTCTACCTTCTTGCAATTAATTTGATTATGT  480
```

```
Query  481   TCTAATGGCATGGCAAGAGAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TCTAATGGCATGGCAAGAGAAATGAAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGT   540

Query  541   TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TTTTGTTGCAGCATACCCTTCTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAG   600

Query  601   TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT   653
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TAGTAGAATACCTCATTGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT   653
```

# Sequence 1192 matched with Sequence 408

```
Query=   Sequence ID 1192
Length=452


   SEQ ID NO: 408

ALIGNMENTS
 Identities = 452/452 (100%), Gaps = 0/452 (0%)

Query  1    GTCTGGAACTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCTGGAACTCCAGACCTCAGGTGATACCCCTGCCTCAGCCTCCCAATGTGCTGGGATTA  60

Query  61   CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAAAAATAAAA  120

Query  121  TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGGACATTCCAAAGT  180

Query  181  AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGTCAACATGCCTCATTCT  240

Query  241  ACCTTCCTCCCTCTGGAATCCAGACACAACTGACCAGCATTAACATTAAAACAGAGATCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACCTTCCTCCCTCTGGAATCCAGACACAACTGACCAGCATTAACATTAAAACAGAGATCT  300

Query  301  TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGTGGGAT  360

Query  361  CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CACCTGAGGTCGGAAGTTCAAGACCAGCCTGGCCGGTATGGTGAAGCCATGTCTCTACTG  420

Query  421  AAAATGCAAAATTGGCCGGACATTGTGGTGCA    452
            ||||||||||||||||||||||||||||||||
Sbjct  421  AAAATGCAAAATTGGCCGGACATTGTGGTGCA    452
```

# Sequence 1193 matched with Sequence 409

Query=  Sequence ID 1193
Length=900


   SEQ ID NO: 409

ALIGNMENTS
 Identities = 900/900 (100%), Gaps = 0/900 (0%)

```
Query  1    TNCNtttttttCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCGGCCGCGTC  64
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TNCNTTTTTTTCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCGGCCGCGTC  64

Query  65   GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT  124
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65   GACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAGAATNGGNCACCT  124

Query  125  GCACNTTTANCCNTGGGTGACAAAANTGAAAACTTTGTCTnaaaaaaaaaaaaaaaaaat  184
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125  GCACNTTTANCCNTGGGTGACAAAANTGAAAACTTTGTCTNAAAAAAAAAAAAAAAAAAT  184

Query  185  tttaantnaaatnaaaaancctttncnttntttttnaaannggggggggNNTTTTTNGGG  244
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  185  TTTAANTNAAATNAAAAANCCTTTNCNTTNTTTTTNAAANNGGGGGGGGNNTTTTTNGGG  244

Query  245  NTTNGNNNTGGTAAAAANTNNNtttttttttttttaggggccnanncccnttttanaaa  304
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  NTTNGNNNTGGTAAAAANTNNNTTTTTTTTTTTTTAGGGGCCNANNCCCCNTTTTANAAA  304

Query  305  anccngnttttnaaaaaantttttttNCCCNCNNTTNgggggggggggNTTTTNANCNNTNT  364
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  ANCCNGNTTTTNAAAAAANTTTTTTNCCCNCNNTTNGGGGGGGGGGGGNTTTTNANCNNTNT  364

Query  365  TNgggggggNNCCCCTNTTANNACCNNCaaanttttttanttttttgnnnaannncccct  424
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365  TNGGGGGGGNNCCCCTNTTANNACCNNCAAANTTTTTANTTTTTTGNNNAANNNCCCCCT  424

Query  425  tttttnnttttttttGNggggggggggNNGCCCCCNNCCTTTNggggggggggNTTNNGn  484
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  425  TTTTTNNTTTTTTTTGNGGGGGGGGGGGNNGCCCCCNNCCTTTNGGGGGGGGGGGNTTNNGN  484
```

```
Query  485  aaaannacttttnaaaannaaGGGNNGGGGGNANATNNccccccccNGGNttttttttttta  544
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  485  AAAANNACTTTTNAAAANNAAGGGNNGGGGGNANATNNCCCCCCCNGGNTTTTTTTTTTA     544

Query  545  aaaantnaanngggggggggnnnctnantnggggcncccanngggggnttanaannaTTTT  604
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545  AAAANTNAANNGGGGGGGGGNNNCTNANTNGGGGCNCCCANNGGGGGNTTANAANNATTTT     604

Query  605  CTNCCCAAACCCCCNGNTTTTATNNccccccccccccNCNNNNGAANGGGNGGNCCNttt   664
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  605  CTNCCCAAACCCCCNGNTTTTATNNCCCCCCCCCCCCNCNNNNGAANGGGNGGNCCNTTT    664

Query  665  tttttatttttNNGGNGGGnaaaaaanttttnaaaaannannaTNTTTTTTccccccccc  724
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  665  TTTTTATTTTTNNGGNGGGNAAAAAANTTTNAAAAANNANNATNTTTTTTCCCCCCCCCC    724

Query  725  ccNCTTTTNGGNAAANCCNNGGGGGGGNTCCTTTTTnaaannnncccccaaaaaaaanttt  784
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  725  CCNCTTTTNGGNAAANCCNNGGGGGGGNTCCTTTTTNAAANNNNCCCCCAAAAAAAANTTT    784

Query  785  ttttnttntnttttctctnggggggnccnnanttntananttttcncnccnaaaaaaaangg  844
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  785  TTTTNTTNTNTTTTCTCTNGGGGNCNNANTTNTANANTTTTNCNCCNAAAAAAAANGG      844

Query  845  gnccccttttttttncngggnnggnncccaaaannttttttttnaaaaaaaaaaaaaa    900
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  845  GNCCCCTTTTTTTNCNGGNNGGNNCCCAAAANNTTTTTTTTNAAAAAAAAAAAAAA       900
```

Blast comparison trimmed "TNCN" from the 5' end of both sequences and reported 896 identities. The report has been manually corrected for this. "TNCN" has been prepended to both sequences and identity count has been increased to 900.

# Sequence 1195 matched with Sequence 410

Query=  Sequence ID 1195
Length=271


   SEQ ID NO: 410

ALIGNMENTS
 Identities = 271/271 (100%), Gaps = 0/271 (0%)

```
Query  1    GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG  60
            ||||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  1    GTTCGTGACNTTCGGAGCTACCTGACAGAGCAGAGTCAACCAGGNTCTGCCCAAAGAGAG  60

Query  61   TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACCTGAGGCCC  120

Query  121  TAGTCTAGCAAGAGGACATAGCACCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGTCTAGCAAGAGGACATAGCACCCTCATCTGGGAATAGGGAAGGCACCTTGCAGAAAA  180

Query  181  TATGAGCAATTTGATATTAACTAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATGAGCAATTTGATATTAACTAACATCTTCAATGTGCCATAGACCTTCCCACAAAGACT  240

Query  241  GTCCAATAATAAGAGATGCTTATCTATTTTA  271
            ||||||||||||||||||||||||||||||||
Sbjct  241  GTCCAATAATAAGAGATGCTTATCTATTTTA  271
```

# Sequence 1196 matched with Sequence 411

Query= Sequence ID - 1196                    nt:      412
Length=412


   SEQ ID NO: 411                  nt:      412

ALIGNMENTS
 Identities = 412/412 (100%), Gaps = 0/412 (0%)

Query  1     GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGAAAAG  60

Query  61    TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGGGAAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAA  120

Query  121   ATTGGTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATTGGTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGC  180

Query  181   TATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGC  240

Query  241   ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACAT  300

Query  301   CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTAAACCTTTTCACCTACAAAATTTCA  360

Query  361   CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT    412
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTGTTTT    412

# Sequence 1197 matched with Sequence 412

Query=   Sequence ID 1197
Length=460


   SEQ ID NO: 412

ALIGNMENTS
 Identities = 460/460 (100%), Gaps = 0/460 (0%)

```
Query  1    CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATCATAG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATCATAG   60

Query  61   AAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGAGA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTGCGAGGAGA   120

Query  121  TCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTCACGCATCTGA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATGTCACGCATCTGA   180

Query  181  TGAAGCGAATTCAGAGAGGCCCAGTAAGAGGTATCTCCATCAAGCTGCAGGAGGAGGAGA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAAGCGAATTCAGAGAGGCCCAGTAAGAGGTATCTCCATCAAGCTGCAGGAGGAGGAGA   240

Query  241  GAGAAAGGAGAGACAATTATGTTCCTGAGGTCTCAGCCTTGGATCAGGAGATTATTGAAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGAAAGGAGAGACAATTATGTTCCTGAGGTCTCAGCCTTGGATCAGGAGATTATTGAAG   300

Query  301  TAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGGACTTCGGCAGTCTGTCCAACCTTC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGGACTTCGGCAGTCTGTCCAACCTTC   360

Query  361  AGGTCACTCAGCCTACAGTTGGGATGAATTTCAAAACGCCTCGGGGACCTGTTTGAATTT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGGTCACTCAGCCTACAGTTGGGATGAATTTCAAAACGCCTCGGGGACCTGTTTGAATTT   420

Query  421  TTTCTGTAGTGCTGTATTATTTTCAATAAATCTGGGACAA    460
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCTGTAGTGCTGTATTATTTTCAATAAATCTGGGACAA    460
```

# Sequence 1198 matched with Sequence 413

```
Query=   Sequence ID 1198
Length=245


   SEQ ID NO: 413

ALIGNMENTS
 Identities = 245/245 (100%), Gaps = 0/245 (0%)

Query  1    CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGGCGAA  60

Query  61   ACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCCTGTAGTCC  120

Query  121  CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGTTGAGGCTGCAGT  180

Query  181  GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTGAGACACCCTGCCTCAG  240

Query  241  AAATA  245
            |||||
Sbjct  241  AAATA  245
```

# Sequence 1199 matched with Sequence 414

Query=  Sequence ID - 1199                    nt:     439
Length=439


   SEQ ID NO: 414               nt:     439

ALIGNMENTS
 Identities = 439/439 (100%), Gaps = 0/439 (0%)

```
Query   1    CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCCAGCC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCCAGCC  60

Query   61   CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATCTTCCACAA  120

Query   121  GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCTGAAGGAGCTGAT  180

Query   181  CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAATTGCAAGGCTGATGGA  240

Query   241  AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGG  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAGGAGTATGTCACCTTCCTGGG  300

Query   301  GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGGCTGAAAATAAATAGGGAAGATGGA  360

Query   361  GACACCCTCTGGGGGTCCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAAtt  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GACACCCTCTGGGGGTCCTCTCTGAGTCAAATCCAGTGGTGGGTAATTGTACAATAAATT  420

Query   421  tttttttGGTCAAATTTAA  439
             |||||||||||||||||||
Sbjct   421  TTTTTTTGGTCAAATTTAA  439
```

# Sequence 1200 matched with Sequence 415

Query=  Sequence ID - 1200                    nt:     526
Length=526


   SEQ ID NO: 415                 nt:     526

ALIGNMENTS
 Identities = 526/526 (100%), Gaps = 0/526 (0%)

```
Query  1    CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAACAGGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAACAGGT  60

Query  61   CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGCCATATCTT  120

Query  121  TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAAGGAAACCATCTG  180

Query  181  CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAATCCTCACCATATGCTGC  240

Query  241  TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAGCTGGGTATCACCGCCCTACA  300

Query  301  CATCAAACTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATCAAACTCCGGGCCACAGGAGGAAATAGGACCAAGACCCCTGGACCTGGGGCCCAGTC  360

Query  361  GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGCCCTCANAGCCCTTGCCCGCTCGGGTATGAAGATCGGGCGGATTGAGGATGTCACCCC  420

Query  421  CATCCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTGGTCGCCGTCTGTGAACAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CATCCCCTCTGACAGCACTCGCAGGAAGGGGGGTCGCCGTGGTCGCCGTCTGTGAACAAG  480
```

```
Query  481  ATTCCTCAAAATATTTTCTGTTAATAAATTGCCTTCATGTAAACTG  526
            ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTCCTCAAAATATTTTCTGTTAATAAATTGCCTTCATGTAAACTG  526
```

# Sequence 1201 matched with Sequence 416

```
Query=  Sequence ID - 1201                    nt:      613
Length=613


   SEQ ID NO: 416                  nt:      613

ALIGNMENTS
 Identities = 613/613 (100%), Gaps = 0/613 (0%)

Query  1    CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCATTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCATTAA  60

Query  61   AATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGATGTCATCAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGATGTCATCAG  120

Query  121  CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGGTCGCTTTGCTGT  180

Query  181  ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAGTGAGAAAGATCTTTGT  240

Query  241  GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCGCACCATCCGCTACCCCGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCCCGCACCATCCGCTACCCCGA  300

Query  301  TCCCCTCATCAAGGTGAATGATACCATTCAGATTGATTTAGAGACTGGCAAGATTACTGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCCCTCATCAAGGTGAATGATACCATTCAGATTGATTTAGAGACTGGCAAGATTACTGA  360

Query  361  TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTCATCAAGTTCGACACTGGTAACCTGTGTATGGTGACTGGAGGTGCTAACCTAGGAAG  420

Query  421  AATTGGTGTGATCACCAACAGAGAGAGGCACCCTGGATCTTTTGACGTGGTTCACGTGAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AATTGGTGTGATCACCAACAGAGAGAGGCACCCTGGATCTTTTGACGTGGTTCACGTGAA  480
```

```
Query  481  AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTTGTTATTGGCAAGGG  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGATGCCAATGGCAACAGCTTTGCCACTCGACTTTCCAACATTTTTGTTATTGGCAAGGG  540

Query  541  CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAACAAACCATGGATTTCTCTTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGA  600

Query  601  GAGAGACAAAAGA  613
            |||||||||||||
Sbjct  601  GAGAGACAAAAGA  613
```

# Sequence 1202 matched with Sequence 417

Query=   Sequence ID 1202
Length=663


   SEQ ID NO: 417

ALIGNMENTS
 Identities = 663/663 (100%), Gaps = 0/663 (0%)

```
Query  1    GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAGAGTG  60

Query  61   ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGTCCCCAAAG  120

Query  121  CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGGTGCTGACTCAGA  180

Query  181  AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGCGCATCATGGCGTGGCA  240

Query  241  AGAGCCTTCGGGTTCAGAAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGAGCCTTCGGGTTCAGAAGATCAGGCCTTCTATCCTGGGCTGCAACATCCTTCGAGTTG  300

Query  301  AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATATTCCTTACTGATCTATGTTAGCGTTCCTGGATCCAAGAAGGTCATCCTTGACCTGC  360

Query  361  CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCTGGTAATTGGCAGCAGATCAGGTCTAAGCAGCAGAACATCCAGCATGGCCAGCCGAA  420

Query  421  CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCCAGAAGCTCCTCCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCAGCTCTGAGATGAGTTGGGTAGATCTGAACATCCCTGATACCCCAGAAGCTCCTCCCT  480
```

```
Query  481  GCTATATGGATGTCATTCCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GCTATATGGATGTCATTCCTGAAGATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAG  540

Query  541  ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATGACATGGATGGCTCTCAAGACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCA  600

Query  601  TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TGCCACCACCGACTTATACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAG  660

Query  661  CAT  663
            |||
Sbjct  661  CAT  663
```

# Sequence 1203 matched with Sequence 418

Query=  Sequence ID - 1203                    nt:      692
Length=692


   SEQ ID NO: 418                   nt:     692

ALIGNMENTS
 Identities = 692/692 (100%), Gaps = 0/692 (0%)

```
Query  1    TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAAACTTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCAGAGGGGTCCATACGGCGTTGTTCTGGATTCCCGTCGTAACTTAAAGGGAAACTTTC  60

Query  61   ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTT  120

Query  121  GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTAT  180

Query  181  AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTG  240

Query  241  CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCC  300

Query  301  AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATT  360

Query  361  GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCTGGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCCA  420

Query  421  CGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCATCTTAT  480
```

```
Query  481  GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTAACCTACCTACCATTGCGCTGTGTAACACAGATTCTCCTCTGCGCTATGTGGACATT  540

Query  541  GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCCATCCCATGCAACAACAAGGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCT  600

Query  601  CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CGGGAAGTTCTGCGCATGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCT  660

Query  661  GATCTGTACTTCTACAGAGATCCTGAAGAGAT  692
            ||||||||||||||||||||||||||||||||
Sbjct  661  GATCTGTACTTCTACAGAGATCCTGAAGAGAT  692
```

# Sequence 1204 matched with Sequence 419

```
Query=  Sequence ID 1204
Length=365


   SEQ ID NO: 419

ALIGNMENTS
 Identities = 365/365 (100%), Gaps = 0/365 (0%)

Query  1    ttttttttttttttCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTTTTTTCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCGCGGC  60

Query  61   CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATCATTGTAGA  120

Query  121  TGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACCCCAGTGCACCTC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACCCCAGTGCACCTC  180

Query  181  CCTGGCCTGGTCTGCTGATGACACAGGTTGGGC  213
            |||||||||||||||||||||||||||||||||
Sbjct  181  CCTGGCCTGGTCTGCTGATGACACAGGTTGGGC  213

Query  214  NGGGNNCNCNGGGGNGGNNNNGNNNNGCNGNNGGNNCNGNNNNCNNNNNGCNNNNGNNNN  272
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  214  NGGGNNCNCNGGGGNGGNNNNGNNNNGCNGNNGGNNCNGNNNNCNNNNNGCNNNNGNNNN  272

Query  273  TNNNCNNNGNNCNNNNNNNNNNNNNNNNNGNTCNNGNNGCNGGGGCCNGGNCGNCGCGG  331
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  273  TNNNCNNNGNNCNNNNNNNNNNNNNNNNNGNTCNNGNNGCNGGGGCCNGGNCGNCGCGG  331

Query  332  NCGCGNNTNNNNGGGTNCNNNCNCNNNGGCGCGC  365
            ||||||||||||||||||||||||||||||||||
Sbjct  332  NCGCGNNTNNNNGGGTNCNNNCNCNNNGGCGCGC  365
```

Blast comparison trimmed
"NGGNNCNCNGGGGNG GNNNNGNNNNGCNGNNGGNNCNGNNNN CNNNNNGC-
NNNNGNNNNTNNNCNNNG NNCNNNNNNNNNNNNN NNNNGNTCNNGNNGC NGGGGC-

CNGGNCGNCGCGGNCG CGNNTNNNNGGGTNCNNNCN CNNNGGCGCGC" from the 3' end of both sequences and reported 213 identities. The report has been manually corrected for this.

"NGGNNCNCNGGGGNGGNNN NGNNNNGCNGNNGGNNCNGNNNN CNNNNNGC-NNNNGNNNNTNNNCNNNG NNCNNNNNNNNNNN NNNNNNGNTCNNGNNGC NGGGGC-CNGGNCGNCGCGGNCG CGNNTNNNNGGGTNC NNNCNCNNNGGCGCGC" has been appended to both sequences and identity count has been increased to 365.

# Sequence 1205 matched with Sequence 420

Query=   Sequence ID 1205
Length=299


   SEQ ID NO: 420

ALIGNMENTS
 Identities = 299/299 (100%), Gaps = 0/299 (0%)

```
Query   1    CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGCATTT   60

Query   61   GCTGAAACTTGaaaaaacaaagcaaatcaaaaacaggaaaaaattgtacctggtactttt   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GCTGAAACTTGAAAAAACAAAGCAAATCAAAAACAGGAAAAAATTGTACCTGGTACTTTT   120

Query   121  ttttagaaaaaaagattaaaaaagaaagaataaattcttgtttggaaacttgaaaaaaaa   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TTTTAGAAAAAAAGATTAAAAAAGAAAGAATAAATTCTTGTTTGGAAACTTGAAAAAAAA   180

Query   181  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaatttttaaactc   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTTAAACTC   240

Query   241  tTNNNNNTNNCNNCNANTAANNCANNTCNANNNNNANNNAATTACTTNNANGTNNNTCACN   299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTNNNNNTNNCNNCNANTAANNCANNTCNANNNNNANNNAATTACTTNNANGTNNNTCACN   299
```


Blast comparison trimmed
"TNNNNNTNNCNNCNANTAANNCANNTCNANNNNNANNNAATTACTTNNANGTNNNTCACN"
from the 3' end of both sequences and reported 241 identities. The report has been man-
ually corrected for this.
"TNNNNNTNNCNNCNANTAANNCANNTCNANNNNNANNNAATTACTTNNANGTNNNTCACN"
has been appended to both sequences and identity count has been increased to 299.

# Sequence 1207 matched with Sequence 421

```
Query=   Sequence ID - 1207                    nt:      642
Length=642


   SEQ ID NO: 421                    nt:      642

ALIGNMENTS
 Identities = 642/642 (100%), Gaps = 0/642 (0%)

Query  1    ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGTGGCA   60

Query  61   AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCATTGCAGCC   120

Query  121  GCAACCCTGTCCTTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCAACCCTGTCCTTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCCATGTATTCCANAA   180

Query  181  AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAGAAAAAGAAGG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTTGAAAAGAAAAAGAAGG   240

Query  241  AGAAGGTTCTCGCAACTGTTACAAAACCAGTTGGTGGTGACAAGAACGGCGGTACCCGGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGAAGGTTCTCGCAACTGTTACAAAACCAGTTGGTGGTGACAAGAACGGCGGTACCCGGG   300

Query  301  TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGTTAAACTTCGCAAAATGCCTAGATATTATCCTACTGAAGATGTGCCTCGAAAGCTGT   360

Query  361  TGAGCCACGGCAAAAAACCCTTCAGTCAGCACGTGAGAAAACTGCGAGCCAGCATTACCC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAGCCACGGCAAAAAACCCTTCAGTCAGCACGTGAGAAAACTGCGAGCCAGCATTACCC   420

Query  421  CCGGGACCATTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCCTGA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCGGGACCATTCTGATCATCCTCACTGGACGCCACAGGGGCAAGAGGGTGGTTTTCCTGA   480
```

Page 707

```
Query  481  AGCAGCTGGCTAGTGGCTTATTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCAGCTGGCTAGTGGCTTATTACTTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTC  540

Query  541  TACGAAGAACACACCAGAAATTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TACGAAGAACACACCAGAAATTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATG  600

Query  601  TAAAAATCCCAAAACATCTTACTGATGCTTACTTCAAAAAGA  642
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TAAAAATCCCAAAACATCTTACTGATGCTTACTTCAAAAAGA  642
```

## Sequence 1208 matched with Sequence 422

Query= Sequence ID 1208
Length=503


   SEQ ID NO: 422

ALIGNMENTS
 Identities = 503/503 (100%), Gaps = 0/503 (0%)

```
Query  1    CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAAAGCT  60

Query  61   AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGT  120

Query  121  AGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGC  180

Query  181  TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCCTCTAAATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCCTCTAAATC  240

Query  241  CCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAAC  300

Query  301  CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAA  360

Query  361  GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATAACTGAACTCCT  420

Query  421  CACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGTATAAGTAACAT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGTATAAGTAACAT  480
```

```
Query  481   GAAAACATTCTCCTCCGCATAAG   503
             |||||||||||||||||||||||
Sbjct  481   GAAAACATTCTCCTCCGCATAAG   503
```

# Sequence 1209 matched with Sequence 423

Query=   Sequence ID - 1209                    nt:      620
Length=620


   SEQ ID NO: 423                nt:     620

ALIGNMENTS
 Identities = 620/620 (100%), Gaps = 0/620 (0%)

```
Query  1    CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG  60

Query  61   TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC  120

Query  121  GCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA  180

Query  181  ACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAGTCTAGGGACAGGAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAGTCTAGGGACAGGAAGA  240

Query  241  TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT  300

Query  301  GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG  360

Query  361  TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG  420

Query  421  TATCCCACGTACTCTATCTTCCATTCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TATCCCACGTACTCTATCTTCCATTCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC  480
```

```
Query  481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGACCTGTATTCCACTTACTCCACCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCC  540

Query  541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT  600

Query  601  TTCTGGTGCTGCTGTGACTT  620
            ||||||||||||||||||||
Sbjct  601  TTCTGGTGCTGCTGTGACTT  620
```

# Sequence 1210 matched with Sequence 424

Query=   Sequence ID 1210
Length=702


   SEQ ID NO: 424

ALIGNMENTS
 Identities = 702/702 (100%), Gaps = 0/702 (0%)

```
Query    1  TTCGTAATTAGAATACTGTTTGGACTTGCTCAACAAGCACCTTATCTTAACAAAAAGTAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  TTCGTAATTAGAATACTGTTTGGACTTGCTCAACAAGCACCTTATCTTAACAAAAAGTAA   60

Query   61  CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT   120

Query  121  CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG   180

Query  181  ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA   240

Query  241  TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA   300

Query  301  ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT   360

Query  361  CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG   420

Query  421  TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA   480
```

Page 713

```
Query  481  CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT  540

Query  541  AGGTGTTTTCACTTGCATTTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGGTGTTTTCACTTGCATTTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT  600

Query  601  ACTACGTTAGGTGTTTTCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACTACGTTAGGTGTTTTCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGC  660

Query  661  TGCCTTATCTAAGGAAGTCCTAAAGTAAATCATTGGAACACA  702
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  TGCCTTATCTAAGGAAGTCCTAAAGTAAATCATTGGAACACA  702
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 1211 matched with Sequence 425

Query=   Sequence ID 1211
Length=632


   SEQ ID NO: 425

ALIGNMENTS
 Identities = 632/632 (100%), Gaps = 0/632 (0%)

```
Query  1    CCATTGTGTTGGNACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCATTGTGTTGGNACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACT  60

Query  61   TTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTATGTGGTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTATGTGGTGG  120

Query  121  CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATG  180

Query  181  GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAA  240

Query  241  CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTA  300

Query  301  TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTTAACAAATTTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAACCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTTAACAAATTTA  360

Query  361  AGACCCTCTCAAACTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGACCCTCTCAAACTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTG  420

Query  421  AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AATAAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTG  480
```

```
Query  481  CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATG  540

Query  541  AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAGGTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAAC  600

Query  601  CAAGAATTGATTGGGCACATCATTTCAAGAAG  632
            ||||||||||||||||||||||||||||||||
Sbjct  601  CAAGAATTGATTGGGCACATCATTTCAAGAAG  632
```

# Sequence 1212 matched with Sequence 426

```
Query=   Sequence ID - 1212                    nt:     374
Length=374


   SEQ ID NO: 426                nt:     374

ALIGNMENTS
 Identities = 374/374 (100%), Gaps = 0/374 (0%)

Query  1    AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCACAAA  60

Query  61   GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGACCAAACAC  120

Query  121  ACCAAGTTCGTGCGGGACATGATTCGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCAAGTTCGTGCGGGACATGATTCGGGAGGTGTGTGGCTTTGCCCCGTACGAGCGGCGC  180

Query  181  GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAAATTTATCAAGAAAAGG  240

Query  241  GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCC  300

Query  301  ATGAGGAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGAGGAAAGCTGCTGCCAAGAAAGACTGAGCCCCTCCCCTGCCCTCTCCCTGAAATAAA  360

Query  361  GAACAGCTTGACAG   374
            ||||||||||||||
Sbjct  361  GAACAGCTTGACAG   374
```

# Sequence 1213 matched with Sequence 427

Query=   Sequence ID - 1213                    nt:     567
Length=567


   SEQ ID NO: 427                  nt:     567

ALIGNMENTS
 Identities = 567/567 (100%), Gaps = 0/567 (0%)

Query  1     GAATTATTGACTTTGAATTGCATTTCAGTACCATGAAGTCAAAGTCAGTGGTGTATTTGC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GAATTATTGACTTTGAATTGCATTTCAGTACCATGAAGTCAAAGTCAGTGGTGTATTTGC   60

Query  61    TCATTTGTTCATTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TCATTTGTTCATTCTTTCTTTTCCACCAACATTACTGCCTGCAGAGCCAGAGGTGAGTGC   120

Query  121   AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACAGCCTACAGTTCC   180

Query  181   ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGGAAATCCTGAATG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGACTTGGAAATCCTGAATG   240

Query  241   GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAAGGCAGAATTCAATAGAACCA   300

Query  301   GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGGAAAAGCTTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGCAGGGGGCAGGGGTGGAAAAGCTTT   360

Query  361   GTACAGGAATTGTGGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTACAGGAATTGTGGAAAAGCTTTTGCATTATCTCTAGTCTGAAAGTCACATTTCTCAGT   420

Query  421   TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCCTTTCCACTCTCTTCTGTCAACTTGCTGTGAGTAAATGACATCTGTCACCTGTGACAC   480

```
Query  481  GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGCCAGGGACTATCACCATATGGCCCCCACACATTATCTAGTACCAGCCTGCCTGGGCC  540

Query  541  ATGCCTTTTCCAGTCACTGTACCAGCC  567
            |||||||||||||||||||||||||||
Sbjct  541  ATGCCTTTTCCAGTCACTGTACCAGCC  567
```

# Sequence 1214 matched with Sequence 428

Query=   Sequence ID - 1214                    nt:      620
Length=620


   SEQ ID NO: 428                  nt:      620

ALIGNMENTS
 Identities = 620/620 (100%), Gaps = 0/620 (0%)

Query  1     CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAGGAAG  60

Query  61    TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGATCCACATCC  120

Query  121   GCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACACCCTCTTCATGA  180

Query  181   ACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAGTCTAGGGACAGGAAGA  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAGTCTAGGGACAGGAAGA  240

Query  241   TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCACCGCCAAGTGCCTGAACATCT  300

Query  301   GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GGGCCCTGATTTTGGGCATCTTCATGACCATTCTGCTCGTCATCATCCCAGTGTTGGTCG  360

Query  361   TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TCCAGGCCCAGCGATAGATCAGGAGGCATCATTGAGGCCAGGAGCTCTGCCCGTGACCTG  420

Query  421   TATCCCACGTACTCTATCTTCCATTCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TATCCCACGTACTCTATCTTCCATTCCTCGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCC  480

```
Query  481   TTGACCTGTATTCCACTTACTCCACCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TTGACCTGTATTCCACTTACTCCACCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCC   540

Query  541   TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TGCATCAGCCCTTTATCCTCACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGT   600

Query  601   TTCTGGTGCTGCTGTGACTT   620
             ||||||||||||||||||||
Sbjct  601   TTCTGGTGCTGCTGTGACTT   620
```

# Sequence 1215 matched with Sequence 429

```
Query=   Sequence ID 1215
Length=669


   SEQ ID NO: 429

ALIGNMENTS
 Identities = 669/669 (100%), Gaps = 0/669 (0%)

Query  1    CACAAGATAGAATGGTaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaTTTTAAGTGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACAAGATAGAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAAGTGA  60

Query  61   CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTGAGTCCAAG  120

Query  121  TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCAGTTTCTCCCAGA  180

Query  181  CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTATTTCAAAGAATCTTTCT  240

Query  241  CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTTAACC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTTGAAAGTTGTTATTGTTAACC  300

Query  301  TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTTAAACATGGTAGTACTGGAAATTTT  360

Query  361  ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAAACTAGTAAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACAAGACTTTTACCTAGCACTTAAATATGTATAAATGTACATAAAGACAAACTAGTAAGC  420

Query  421  ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATGACCTGGGGAAATGGTCAGACCTTGTATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGA  480
```

```
Query   481   CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   CCAGAATCTGCCATGGCAACAGGCTTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACT   540

Query   541   GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTTCTAAGACTGA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   GTGGTGTTAGCACCAGCCAGCTCTCTGTACATTTGCTAGCTTGTAGTTTTCTAAGACTGA   600

Query   601   GTAAACTTCTTATTTTTAGAAAGTGGAGGTCTGGTTTGTAACTTTCCTTGTACTTAATTG   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   GTAAACTTCTTATTTTTAGAAAGTGGAGGTCTGGTTTGTAACTTTCCTTGTACTTAATTG   660

Query   661   GGTAAAAGT   669
              |||||||||
Sbjct   661   GGTAAAAGT   669
```

# Sequence 1216 matched with Sequence 430

```
Query=  Sequence ID - 1216                    nt:     484
Length=484


   SEQ ID NO: 430                 nt:     484

ALIGNMENTS
 Identities = 484/484 (100%), Gaps = 0/484 (0%)

Query  1    CAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCTGGCG  60

Query  61   CAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAATATAGCAAG  120

Query  121  GACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGAGAGCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGAGAGCC  180

Query  181  AAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCCGT  240

Query  241  CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGCCTGGT  300

Query  301  GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCCTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAACCCTC  360

Query  361  TAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACACTAGGA  420

Query  421  AAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAGCCACC  480
```

```
Query  481  AATT  484
            ||||
Sbjct  481  AATT  484
```

# Sequence 1217 matched with Sequence 431

Query=   Sequence ID 1217
Length=576


   SEQ ID NO: 431

ALIGNMENTS
 Identities = 576/576 (100%), Gaps = 0/576 (0%)

```
Query  1    GACAGGCGGGGCCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAGGCGGGGCCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGAGAGT  60

Query  61   CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTCAAGGAGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTCAAGGAGTC  120

Query  121  AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAAACTTCTTGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTAAAACTTCTTGAT  180

Query  181  AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAGAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGAAACAGTAGTGGAGAAT  240

Query  241  CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACTTGACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGAAGAGAGTTGAAAACTTGACT  300

Query  301  TTTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCCTCATAGGTAGCAGAGTTTTCAGGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCCTCATAGGTAGCAGAGTTTTCAGGT  360

Query  361  TTTCCTCTTAGCTATCCAAATACTaaaaaaaaTTCTGATATACGAACCTTTTTTCATAATA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTCCTCTTAGCTATCCAAATACTAAAAAAATTCTGATATACGAACCTTTTTTCATAATA  420

Query  421  CAGGTTTTAATTATATTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CAGGTTTTAATTATATTTTTCATTCAGATACACAGTAGATCTTAAATATAGAAAGTTTTT  480
```

```
Query  481  GTTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTTTACTTAAATCTATTTGGAAGTTTATATTTGAGCTAATAATTAAGCTGGAGCATGTAT  540

Query  541  AATAGATTTAAATTGTTTTGACTGTTAGTGAAATTT  576
            ||||||||||||||||||||||||||||||||||||
Sbjct  541  AATAGATTTAAATTGTTTTGACTGTTAGTGAAATTT  576
```

# Sequence 1218 matched with Sequence 432

Query=   Sequence ID 1218
Length=669


   SEQ ID NO: 432

ALIGNMENTS
 Identities = 669/669 (100%), Gaps = 0/669 (0%)

```
Query  1    CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGATTTT  60

Query  61   ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCCTGTCTGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCCTGTCTGAA  120

Query  121  CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAGGCAGCCAGGAGC  180

Query  181  AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAATAAACTCCTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGGGAAAATAAACTCCTTC  240

Query  241  CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACTCAAGCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCAACTTCAATCCAACTCAAGCA  300

Query  301  TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCTGGGGCTGAACTTCTTCCTATAACT  360

Query  361  TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTTGAAACAACAAGAACTCAAGGTGTGACAGTTACAAGTGGGCCCTTTTTCACAGTGTG  420

Query  421  TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TACCTAAACACGTGAGGACCCTGGATTACAGAATGACAGACTCGAAGTGACTCAAGTTCC  480
```

```
Query  481  GGTTGTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGTTGTTCATCTTTAGATGGTAAAGATGGCTGTACGTACTATCCTTGCTTATTTCCAATC  540

Query  541  TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TATTGTTTAAACTCTTGTATATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAA  600

Query  601  ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTTGAATG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ATGAGTGAATTCAAGTAATCCATTACTAATGTGATCTGGAAACAAACATGGTGTTGAATG  660

Query  661  TGCATATGT  669
            |||||||||
Sbjct  661  TGCATATGT  669
```

# Sequence 1219 matched with Sequence 433

Query=   Sequence ID - 1219                    nt:     559
Length=559


   SEQ ID NO: 433                 nt:     559

ALIGNMENTS
 Identities = 559/559 (100%), Gaps = 0/559 (0%)

```
Query  1    CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTGGAGA   60

Query  61   TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAGGTAAACTG   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAGGTAAACTG   120

Query  121  AGGCACAATGCAAttttttttttttttttAAGGAGTTTATTTGAGCAAACAGTGATTCATG   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGCACAATGCAATTTTTTTTTTTTTTTTAAGGAGTTTATTTGAGCAAACAGTGATTCATG   180

Query  181  AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGATGAGGGACAAGCATTT   240

Query  241  ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAACCGGGTGCGGTGGCTTACAC   300

Query  301  TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCAGATCACAAGATCAAGAGATCGAGA   360

Query  361  CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCATCCTGGTCAACATGGTGAAACCCCATCTNTACTAAAAAATACAAAAATTANCTGGGC   420

Query  421  GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGGTGGTGCGTGCCTGTAGTCCCAGCTACTTGGGCGGCTGAGGCAGGANAATTGCTTGA   480
```

```
Query   481   ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   ACCCGGGAGGTGGAGGTTGCAGTAAGCCGAGATTGCACCATTGCACTACTCCAGCCTGGT   540

Query   541   GACAGAGAGAGACTCCATC   559
              |||||||||||||||||||
Sbjct   541   GACAGAGAGAGACTCCATC   559
```

# Sequence 1220 matched with Sequence 434

Length=1354
 Identities = 1354/1354 (100%), Gaps = 0/1354 (0%)

```
Query  1    GANNNGTGCGATANNATGNNTGTCtttttttttAAAGTNTTTCNNATNGNAGNGAANCCCCNNAN   65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GANNNGTGCGATANNATGNNTGTCTTTTTTTTAAAGTNTTTCNNATNGNAGNGAANCCCCNNAN   65

Query  66   NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT   125
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  66   NTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATAGTAGTANCAANAT   125

Query  126  TGTNTTAGCTANATNANTCAATAGATATCNAGATanaanaananCNNGGATATACAGCGA   185
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  126  TGTNTTAGCTANATNANTCAATAGATATCNAGATANAANAANANCNNGGATATACAGCGA   185

Query  186  TGTNTNANNGGnnnnnnnanGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG   245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  TGTNTNANNGGNNNNNNNANGGAACGAACATCNACNTTAANNATAAGCTNGNGGAGAGAG   245

Query  246  ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGnnnnnnnannTANTAT   305
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  246  ACANGTANGTTATANANNAGAATNGNAGTAGGNGTGATCATAATAGNNNNNANNTANTAT   305

Query  306  ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN   365
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  306  ATANGATNTTANTGNNCTNTNNTNNGTTTATCNNNAATNTCTATNCTNGAGAGNAGCNNN   365

Query  366  ATNNNNAGGCGANGANATTGGGNNNTNCTCNTNATAGANANCTGGTGTCnnanaantacn   425
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  366  ATNNNNAGGCGANGANATTGGGNNNTNCTCNTNATAGANANCTGGTGTCNNANAANTACN   425

Query  426  tcatctattnanctctcacnanatggnannatanagnagngnnntnnanaggantangca   485
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  426  TCATCTATTNANCTCTCACNANATGGNANNATANAGNAGNGNNNTNNANAGGANTANGCA   485

Query  486  tagngnntnnctnaaacaaaannnataaganntctcgnnaananGGGCCTNTNNTNTAGC   545
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  486  TAGNGNNTNNCTNAAACAAAANNNATAAGANNTCTCGNNAANANGGGCCTNTNNTNTAGC   545

Query  546  GAGGNNTTANTTTNTATANTTNTTCNCTCTtnnaatanntangatanatganctngnngt   605
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  546  GAGGNNTTANTTTNTATANTTNTTCNCTCTTNNAATANNTANGATANATGANCTNGNNGT  605

Query  606  gatanatannnnntacngtnaanntntantcntataatagatanaaatataggatntTNC  665
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  606  GATANATANNNNNTACNGTNAANNTNTANTCNTATAATAGATANAAATATAGGATNTTNC  665

Query  666  TCTGGCNGGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTnana  725
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  666  TCTGGCNGGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTNANA  725

Query  726  nnnnnTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTTT  785
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  726  NNNNNTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTTT  785

Query  786  GTATNAATATnaaanaaGGTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAATTAGC  845
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  786  GTATNAATATNAAANAAGGTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAATTAGC  845

Query  846  ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN  905
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  846  ATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAGNAGTCATTN  905

Query  906  NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCagantatattntgngaanatga  965
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  906  NGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCAGANTATATTNTGNGAANATGA  965

Query  966  anntacgnantcctnngnantatnatnnntgantanganaancnananntnttntannant  1025
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  966  ANNTACGNANTCCTNNGNANTATNATNNTGANTANGANAANCNANANNTNTTNTANNANT  1025

Query  1026 gnctatanattgccnngatanattntnnnaatgaanCGATAGCCCGCNCTAAGGanntnn  1085
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1026 GNCTATANATTGCCNNGATANATTNTNNNAATGAANCGATAGCCCGCNCTAAGGANNTNN  1085

Query  1086 gtnanntaaanntctcagataanntacntnttnnttattaancnannatcacantatanC  1145
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1086 GTNANNTAAANNTCTCAGATAANNTACNTNTTNNTTATTAANCNANNATCACANTATANC  1145

Query  1146 NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC  1205
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1146 NGNGACANNNGCGANANTATATGTATGNNANTATNACNGNTCCNNNCCGNGAANNTANTC  1205
```

Page 733

```
Query  1206  NTANNAGGCATTCNGNNGAGCTNTTCTNCTAGACNATTTnnantgaaannatgcngnnaa  1265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1206  NTANNAGGCATTCNGNNGAGCTNTTCTNCTAGACNATTTNNANTGAAANNATGCNGNNAA  1265

Query  1266  aaaCGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN  1325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1266  AAACGACNNNCTTNAANTTNTGTCTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGN  1325

Query  1326  NNANTNANNGCTCTCANCTNGCTNNNACT  1354
             |||||||||||||||||||||||||||||
Sbjct  1326  NNANTNANNGCTCTCANCTNGCTNNNACT  1354
```

Blast comparison trimmed "GANNN" from the 5' end of both sequences and trimmed
"NNNACT" from the 3' end of both sequences and reported 1343 identities. The report
has been manually corrected for this. "GANNN" has been prepended to the 5' end of both
sequences and "NNNACT" has appended to the 3' end of both sequencies and identity
count has been increased to 1354.

# Sequence 1221 matched with Sequence 435

```
Query=   Sequence ID - 1221                    nt:      741
Length=741


   SEQ ID NO: 435                  nt:     741

ALIGNMENTS
 Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query  1    AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA  60

Query  61   CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCACTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCACTGG  120

Query  121  TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC  180

Query  181  CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT  240

Query  241  AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACTTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACTTTG  300

Query  301  TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT  360

Query  361  ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC  420

Query  421  TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA  480
```

```
Query  481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540

Query  541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600

Query  601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660

Query  661  CTAATTTGAGATCACCTAAACACTGGAAAAGaaaaaaaaTGAAAGGGCAGTATGTCCATA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CTAATTTGAGATCACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATA  720

Query  721  AACCAACAAATAATTTGGCTG  741
            |||||||||||||||||||||
Sbjct  721  AACCAACAAATAATTTGGCTG  741
```

# Sequence 1224 matched with Sequence 436

```
Query=   Sequence ID - 1224                    nt:      485
Length=485


   SEQ ID NO: 436               nt:     485

ALIGNMENTS
 Identities = 485/485 (100%), Gaps = 0/485 (0%)

Query  1    CGAAATTTCCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAAATTTCCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGA  60

Query  61   GTATTTCAGGGTTCACTTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTATTTCAGGGTTCACTTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCC  120

Query  121  AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAGGAAGCTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAGGAAGCTT  180

Query  181  CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGT  240

Query  241  GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC  300

Query  301  TGCACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCACCACACAATCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGAGATTGGCTT  360

Query  361  GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTCGTTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGTTCTTCATGAGCACATTTGATATAGCTCTTTTTCTGTTTTTCCTTGCTCATTTCGTTT  420

Query  421  TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGGGAAGAAATCTGTACTGTATTGGGATTGTAAAGAACATCTCTGCACTCAGACAGTTT  480
```

```
Query  481  ACAGA  485
            |||||
Sbjct  481  ACAGA  485
```

# Sequence 1226 matched with Sequence 437

```
Query=  Sequence ID 1226
Length=637


   SEQ ID NO: 437

ALIGNMENTS
 Identities = 637/637 (100%), Gaps = 0/637 (0%)

Query  1    GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCCCACT  60

Query  61   TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGGGCAATGTC  120

Query  121  TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACTCCCGGTTCCCCGAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACTCCCGGTTCCCCGAG  180

Query  181  AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCTCTCCTAGCCATGCAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCTCTCCTAGCCATGCAGG  240

Query  241  CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCTGTCTGAATCCGGCTGAGGGG  300

Query  301  TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGATGGCAGGGTGGGTGACTCCAACCA  360

Query  361  CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCTCTGCCTGTGGTAGCCAGATGGGCCACACCTGCTAGAGCTTCCAGCCCAGCAGTCCCG  420

Query  421  CTACTCTGTGGGTGGGTGCCATCCCCTGTTCCTCTGGGAAGCACCCAGACAGCTGATTAC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTACTCTGTGGGTGGGTGCCATCCCCTGTTCCTCTGGGAAGCACCCAGACAGCTGATTAC  480
```

```
Query   481  GTGACCCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  GTGACCCCACCCACTTCTGCAGATCCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCC   540

Query   541  CAAGCAGGGAAGAGCCCTCATTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA   600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  CAAGCAGGGAAGAGCCCTCATTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTA   600

Query   601  NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT   637
             |||||||||||||||||||||||||||||||||||||
Sbjct   601  NGCTGGTGGAGGAGTGAGGTGGAGGAGGTATGCCTCT   637
```

# Sequence 1228 matched with Sequence 438

Query=   Sequence ID 1228
Length=420


   SEQ ID NO: 438

ALIGNMENTS
 Identities = 420/420 (100%), Gaps = 0/420 (0%)

```
Query  1    GTTATTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAAACATCGGCTCACACCTGTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTATTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAAACATCGGCTCACACCTGTA  60

Query  61   ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTTCGAGACCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTTCGAGACCA  120

Query  121  GCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACATTAGCTGGGTGTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACATTAGCTGGGTGTA  180

Query  181  GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAATGGCTTGAACC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAGGAAAATGGCTTGAACC  240

Query  241  TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGCACTCCAGCCTGGGCGACAGA  300

Query  301  GCGAGACTCCATCTCAAAAGAAGaaaaaaaaaaacaacaaaaaaaCCTTTATCAGATTATC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCGAGACTCCATCTCAAAAGAAGAAAAAAAAAAACAACAAAAAAACCTTTATCAGATTATC  360

Query  361  AGAGGTTATCACTACAGAGGGAGGTAAAATTGGAGGGAAAAGGGTACAAATTTATTTCAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGAGGTTATCACTACAGAGGGAGGTAAAATTGGAGGGAAAAGGGTACAAATTTATTTCAC  420
```

# Sequence 1230 matched with Sequence 439

```
Query=   Sequence ID - 1230                   nt:      741
Length=741


   SEQ ID NO: 439                  nt:      741

ALIGNMENTS
 Identities = 741/741 (100%), Gaps = 0/741 (0%)

Query  1    AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGAGCCA  60

Query  61   CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCACTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCATTTCACTGG  120

Query  121  TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACATTCCAGTAAGAAC  180

Query  181  CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAGGGGCAGTAAGGTTAGT  240

Query  241  AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACTTTG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTACAATAACACAAACAACTTTG  300

Query  301  TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAAGGCCATGTTTTATTTGCTGATTAATGGACAAAAGGCAATGTAATTTATTTTCAAGT  360

Query  361  ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTTTCTTGAAAGTCTGTGCTCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCAC  420

Query  421  TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGAAACTTCAAATATATCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAA  480
```

```
Query  481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATAAAGCAATCATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATA  540

Query  541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAAGTTTCTCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATT  600

Query  601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCAAAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC  660

Query  661  CTAATTTGAGATCACCTAAACACTGGAAAAGaaaaaaaaTGAAAGGGCAGTATGTCCATA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CTAATTTGAGATCACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATA  720

Query  721  AACCAACAAATAATTTGGCTG  741
            |||||||||||||||||||||
Sbjct  721  AACCAACAAATAATTTGGCTG  741
```

# Sequence 1231 matched with Sequence 440

```
Query=   Sequence ID - 1231                  nt:     203
Length=203


   SEQ ID NO: 440              nt:     203

ALIGNMENTS
 Identities = 203/203 (100%), Gaps = 0/203 (0%)

Query  1     TTGAGGAAGGGTCTACTGTCTTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TTGAGGAAGGGTCTACTGTCTTTTTAAATGGCACAATTTTAAGAGGTTTGAGAGGTACAG   60

Query  61    TCCCTTAACCTGCCACGGGAGAGGGGCCCCCAAACTTTCTTCCCCCCACACTTCTGGTTT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TCCCTTAACCTGCCACGGGAGAGGGGCCCCCAAACTTTCTTCCCCCCACACTTCTGGTTT   120

Query  121   TCTGTGTGGAGGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TCTGTGTGGAGGGGGAGCAGGGATATCTAAGCTGTGGTGTGAAAGGGTAGGAGAGATGCT   180

Query  181   GGAGGTGGGGGTGCTGTGTTCTA   203
             |||||||||||||||||||||||
Sbjct  181   GGAGGTGGGGGTGCTGTGTTCTA   203
```

# Sequence 1239 matched with Sequence 441

Query=   Sequence ID 1239
Length=874


   SEQ ID NO: 441

ALIGNMENTS
 Identities = 874/874 (100%), Gaps = 0/874 (0%)

```
Query  1    TTTCCTCGGGAAGCGCGCCATTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACAttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTCCTCGGGAAGCGCGCCATTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACATTT  60

Query  61   ttttttttttttttttttAGAATGATTAACAATTTATTGAGTTTTATTTATCTACAAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTTTTTTTTTTTTTTTTAGAATGATTAACAATTTATTGAGTTTTATTTATCTACAAAAA  120

Query  121  TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTCAGTACCTGAACTGGCTACAAC  180
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATAGCAATACAGNGAACTTCACCAAATCCTAAATATTCAGTACCTGAACTGGCTACAAC  180

Query  181  ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGCAGATATGGGAGAGTCAGCCAGTGA  240
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCGNGTGCACACCCAGTTCCTGCAGAATCTCTTGCAGATATGGGAGAGTCAGCCAGTGA  240

Query  241  AAAGATCCATTTCTTGGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAAGATCCATTTCTTGGGAATCCTTGTCAACAAGACCAGTTCAGAAATCCAGGATATATA  300

Query  301  GAAGCCTACTGTAATTTaaaaacagtaacaaaaaccccaacaaaacccaaatcaacaaaG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAAGCCTACTGTAATTTAAAAACAGTAACAAAAACCCCAACAAAACCCAAATCAACAAAG  360

Query  361  ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCCTTTACATGCAATACATG  420
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACCAAGATAAAGGNGTGATAAACATTAATTGTAATGGTTTTCCTTTACATGCAATACATG  420

Query  421  CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  421  CATTTTAAAATCACTAAGAAACACGAAATTTTGTAGAGCAAAGTTTGNGTTTCACGTAAG  480
```

```
Query  481   TGCAAATGAatatatattttatttttttatactattaaattatatatattttttCCATACA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TGCAAATGAATATATATTTTATTTTTTATACTATTAAATTATATATATTTTTTCCATACA   540

Query  541   AAAGCACACAGTGTTAATCTATAAAATGACATCCAAGTGGATGATGATTGTTTTTGCATG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AAAGCACACAGTGTTAATCTATAAAATGACATCCAAGTGGATGATGATTGTTTTTGCATG   600

Query  601   TCCCCCTGCTTAGAtttttttaaaatatatagtcaaaaattaacatccttctttaaaaat   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TCCCCCTGCTTAGATTTTTTTAAAATATATAGTCAAAAATTAACATCCTTCTTTAAAAAT   660

Query  661   acagaagggaaaaangggcaaaaaaaaaaaTCTAGACTCGAGCAAGCTTATGCATGCATG   720
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   ACAGAAGGGAAAAANGGGCAAAAAAAAAAATCTAGACTCGAGCAAGCTTATGCATGCATG   720

Query  721   CGGCCGCAATTCGANCTCGGNCGACTTGGCCAATTCGCCCTATAGNGAGTCGNATTACAA   780
             |||||||||||||| |||||| ||||||||||||||||||||||| ||||||||||||||
Sbjct  721   CGGCCGCAATTCGANCTCGGNCGACTTGGCCAATTCGCCCTATAGNGAGTCGNATTACAA   780

Query  781   TTCACTGGGCCGNCGNTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCNNCTNA   840
             ||||||||||||| ||| ||||||| |||||||||||||||||||||||||||||||| |
Sbjct  781   TTCACTGGGCCGNCGNTTTACAACGTCGNGACTGGGAAAACCCTGGCGTTACCCNNCTNA   840

Query  841   TCGNCTTGNAACAATNCCCNTTTNGCCAGNGGGG   874
             |||||||||||||||||||| ||||||||||||
Sbjct  841   TCGNCTTGNAACAATNCCCNTTTNGCCAGNGGGG   874
```

# Sequence 1255 matched with Sequence 442

Query=   Sequence ID 1255
Length=928


   SEQ ID NO: 442

ALIGNMENTS
 Identities = 928/928 (100%), Gaps = 0/928 (0%)

```
Query    1   TCACTTCGTATNGAANCTGTTTGGACTTGCTCAACAAGACCTTATCTTAACAAAAAGTAA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1   TCACTTCGTATNGAANCTGTTTGGACTTGCTCAACAAGACCTTATCTTAACAAAAAGTAA   60

Query   61   CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   CTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAAAGCTGACT   120

Query  121   CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGGACTTTTTAAGGGCCGGAAGGG   180

Query  181   ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAGGAAACTGAGGCCTAGA   240

Query  241   TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAGTAGTCTATCCGTAAGAGACA   300

Query  301   ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ACATGGAGAAAGAAATACAACGTTTTTATAGTGAATTATCATCTTACAAAGAATATTCTT   360

Query  361   CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCCATATCGCACTTTTAAAAAGTGGGTACCTTAGTCAAATAGGAGAAAAAACCACTTGAG   420

Query  421   TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TAGTTTCATCCTCAGGTTTTAGGTGAGGAAACTGATACTCAGATTAAATAACTTTAAGCA   480
```

```
Query  481   CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CACAGAGCCTGAATGATAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTT   540

Query  541   AGGTGTTTTCACTTGCATTTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGGTGTTTTCACTTGCATTTCCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGT   600

Query  601   ACTACGTTAGGTGTTTTCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ACTACGTTAGGTGTTTTCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGC   660

Query  661   TGCCTTATCTAAGNAGTCCTAAAGTAAATCATTGGAACACATGTANCCAGTTTGTTGTTT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TGCCTTATCTAAGNAGTCCTAAAGTAAATCATTGGAACACATGTANCCAGTTTGTTGTTT   720

Query  721   TTATTTGCCAGGTNTCAAATATAACTGAAAACCCATGCTAACTGACTNATTTTAAAAGNT   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TTATTTGCCAGGTNTCAAATATAACTGAAAACCCATGCTAACTGACTNATTTTAAAAGNT   780

Query  781   GTNTGGGGCATGAAANGATTGCTCTGCCTGGGCGGGNGGTTNANCCTGNGTCCCCCNTTT   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   GTNTGGGGCATGAAANGATTGCTCTGCCTGGGCGGGNGGTTNANCCTGNGTCCCCCNTTT   840

Query  841   NGGAGNCCACCCANGANGCGATATTTNAGGGNNGATTCNAAACCCCTGGCACGNGNNAAC   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   NGGAGNCCACCCANGANGCGATATTTNAGGGNNGATTCNAAACCCCTGGCACGNGNNAAC   900

Query  901   CCCNTTTTTAAAANANAAAAANANCGGNNG   928
             ||||||||||||||||||||||||||||||
Sbjct  901   CCCNTTTTTAAAANANAAAAANANCGGNNG   928
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 1256 matched with Sequence 443

Query=   Sequence ID 1256
Length=954


   SEQ ID NO: 443

ALIGNMENTS
 Identities = 954/954 (100%), Gaps = 0/954 (0%)

```
Query  1    TTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACTTTA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTACACTTTA   60

Query  61   ATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTATGTGGTGGCTT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTATGTGGTGGCTT   120

Query  121  TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATGGAA   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAACTAGAAATGAATGGAA   180

Query  181  GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGATTGCAACTGTAGGGAACAC   240

Query  241  CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CATTTATGCAGTGGGAGGATTCGATGGCAATGAATTTCTGAATACGGTGGAAGTCTATAA   300

Query  301  CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTTAACAAATTTAAGA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTTGAGTCAAATGAATGGAGCCCCTATACAAAGATTTTCCAGTTTTAACAAATTTAAGA   360

Query  361  CCCTCTCAAACTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCTCTCAAACTAACAGGCTTAGTGATGTAATTATGGTTAGCAGAGGTACACTTGTGAAT   420

Query  421  AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAAGAGGGTGGGTGGGTATAGATGTTGCTAACAGCAACACAAAGCTTTTGCATATTGCAT   480
```

```
Query   481   ACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   ACTATTAAACATGCTGTACATACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAG   540

Query   541   GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   GTCTGTTTTGTGTACTTTTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAA   600

Query   601   GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTTGTTTTGCCAATT   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   GAATTGATTGGGCACATCATTTCAAGAAGTCCCCTCTCCTCCACATTTGTTTTGCCAATT   660

Query   661   TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   TGCACATTAAATGACTCTTCCCTCAAATGTGTACTATGGGGTAAAAGGGGTAGGGNTTAA   720

Query   721   ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTCATAACTGGAACACTCTNTACAAG   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721   ANATGTAAACAGTTGGGTTTTTTAAGGGNCCTTTTTCATAACTGGAACACTCTNTACAAG   780

Query   781   GNTNCTTNTTAAATAAATAACTTGACTTTTTTGTTTTNTAAANGNANCTTCNTGCTTCCA   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781   GNTNCTTNTTAAATAAATAACTTGACTTTTTTGTTTTNTAAANGNANCTTCNTGCTTCCA   840

Query   841   TaaaaaaaaaaaTTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA   900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841   TAAAAAAAAAAATTTAANTNGNCANCTNTGCTGCTGCGNCCANTTNGCTNGNCCNTGGCA   900

Query   901   TTCCCTAGGGANGNTNAATANTGGCNNNTTAACNNGGCNGNAACNNNNNCCANT    954
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   901   TTCCCTAGGGANGNTNAATANTGGCNNNTTAACNNGGCNGNAACNNNNNCCANT    954
```

Blast comparison trimmed "NNNTTAACNNGGCNGNAACNNNNNCCANT" from the 3'
end of both sequences and reported 925 identities. The report has been manually corrected
for this. "NNNTTAACNNGGCNGNAACNNNNNCCANT" has been appended to both
sequences and identity count has been increased to 954.

# Sequence 1331 matched with Sequence 444

```
Query=   Sequence ID 1331
Length=787


   SEQ ID NO: 444

ALIGNMENTS
 Identities = 787/787 (100%), Gaps = 0/787 (0%)

Query  1    GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGGCGATGCATGCTTTATTAAGGCTCTTGTTTCACCTGGCAGTGTACTGTATCAACGTAT  60

Query  61   AATACAGaaaaaaaaTCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATACAGAAAAAAAATCTCTTTAAGGTCCTCCTTCACAAAGACATAGAGTGAAACTCCCT  120

Query  121  TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTTAAAATGGAAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTACATGTCAGTATTTGTTCAACACTTTAGGCAACTTGACTGTCAGTGTTAAAATGGAAA  180

Query  181  ACAGGAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACAGGAAAATGGAAAAATCTGACCAATTCTGCCACCTTGAGACTTTCATATAGACCTTGC  240

Query  241  ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACAACAATTGTATAGATCACACACCGGCTGTATTTAATATGTAACATTTTCACACATATT  300

Query  301  AAAGATACAGAAGTATTAAAAAACCCCCAATGTTAATGTATTTGCTTAAAAGGCACAAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAGATACAGAAGTATTAAAAAACCCCCAATGTTAATGTATTTGCTTAAAAGGCACAAGT  360

Query  361  TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTCACATATCTGTCTAGCTATCTGTTGGTAATACAGAAAGTATACTACTTTTTTAAAAAA  420

Query  421  GTGGGCAGAATTCTtgtgtatgtatatttgtgtgtacagtatgtgtatgtgtgtatatat  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGGGCAGAATTCTTGTGTATGTATATTTGTGTGTACAGTATGTGTATGTGTGTATATAT  480
```

```
Query  481   atatattatatatatagataatatataaaatattttttttAAGGAGAAACTAGAATGTTTA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATATATTATATATATAGATAATATATAAATATTTTTTTTAAGGAGAAACTAGAATGTTTA   540

Query  541   GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAAATGGCCATAAAGGAGGTAAAAA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GCTAGAAAATTCCACAGCCTGTGAAGAAATATTTCAAAATGGCCATAAAGGAGGTAAAAA   600

Query  601   TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TGAAAACCATAACCTAACTTTTATAGAGGCTTTATCTTTAATTTAACGATGTGCGGAGGA   660

Query  661   CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CTTTCTTGCTTGAATCTGTTCCGGGCTGTCTGCTCTGTCCATCAAATGGGCAGGTCTGGG   720

Query  721   AATGAGGCACCTTCGGCCGTTCAGAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AATGAGGCACCTTCGGCCGTTCAGAAGTGGCCTGAACAGAATGCTGGAACCCAGGCTGGA   780

Query  781   CTCGGAC   787
             |||||||
Sbjct  781   CTCGGAC   787
```

# Sequence 1332 matched with Sequence 445

Query=   Sequence ID 1332
Length=689


   SEQ ID NO: 445

ALIGNMENTS
 Identities = 689/689 (100%), Gaps = 0/689 (0%)

```
Query    1  CAAACCTGCATGTTCTGCACATGTATCCAGGAACTTAAAAAAAAAAAAGATAGTTTGTG   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  CAAACCTGCATGTTCTGCACATGTATCCAGGAACTTAAAAAAAAAAAAGATAGTTTGTG   60

Query   61  TGTCTTAATTGAATAATAGTAGATTTATAGATTAAAGATCTATGGGTTTTTAATATGGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  TGTCTTAATTGAATAATAGTAGATTTATAGATTAAAGATCTATGGGTTTTTAATATGGAT  120

Query  121  TAGAAATCTGTGGGTTTTTGATATGGATTAGAAATCTGTGGGTTTTTAATATGGATTGGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAGAAATCTGTGGGTTTTTGATATGGATTAGAAATCTGTGGGTTTTTAATATGGATTGGA  180

Query  181  AATCTGTGGGTTTTTAATATGGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAAC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATCTGTGGGTTTTTAATATGGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAAC  240

Query  241  ATCTGTGGGTTTTTAATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATCTGTGGGTTTTTAATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGT  300

Query  301  GGGTTTTTAATATGGGTTAAAAATCAAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGGTTTTTAATATGGGTTAAAAATCAAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAA  360

Query  361  ATACAGGCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATACAGGCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTT  420

Query  421  GAAGAAGAGAATAAGGTGCTAGCATTCCTATCCGTAGATAATTTGACAGCTAGGAAATAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAAGAAGAGAATAAGGTGCTAGCATTCCTATCCGTAGATAATTTGACAGCTAGGAAATAG  480
```

```
Query  481   GGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGCAGTTATCGTAGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGCAGTTATCGTAGA   540

Query  541   AGAGTACTCAAAAAAATCTGTAAAAAATAAAGAAAGGCCGGGCGCGGTGGCTCACGCCTG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGAGTACTCAAAAAAATCTGTAAAAAATAAAGAAAGGCCGGGCGCGGTGGCTCACGCCTG   600

Query  601   TAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAGGAGATCGAGACCA   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAGGAGATCGAGACCA   660

Query  661   TCCTGGCTACCANGGTGAAACCCCCGTCT   689
             |||||||||||||||||||||||||||||
Sbjct  661   TCCTGGCTACCANGGTGAAACCCCCGTCT   689
```

The two sequences have been compared manually and found to be 100% identical. The two sequences were then split in chunks of 60 base pairs and the comparison formatted as a blast search result.

# Sequence 1335 matched with Sequence 446

Query=  Sequence ID 1335
Length=688


   SEQ ID NO: 446

ALIGNMENTS
 Identities = 688/688 (100%), Gaps = 0/688 (0%)

```
Query  1    CAAGACTCCATCTCaaaaaaaaaaaaaaaTCTACAGTGCTGAGTATATAAAATTATTAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTATTAAC  60

Query  61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAACAGGTAAT  120

Query  121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATTTTAAATGTTAAT  180

Query  181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTGTTTTTTATTTAAATTT  240

Query  241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGTTCCTCTGTAAACTAAAAGAACACGAAGTAATTGGTCACAATTACTGGTGTTTAACT  300

Query  301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAATATTTAGTCCTTCTGAGATGGCTT  360

Query  361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAATATTTGAATTTTGTTGTACGTCTATACTGGGTAGTCACAAGTCTTATAAACACTTTA  420

Query  421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGGAAAGATGGATTTCAGTCTGTATTTTTAAACATCATTTATTTTAAATCTGGTGCTGA  480
```

```
Query   481  AAAATAAGaaaaaaaTTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAA  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AAAATAAGAAAAAAATTAAACTGCATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAA  540

Query   541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATACTGCTGTAATACTGTCATGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCA  600

Query   601  GTGttttttttgtttttttCCTAGAAATGTTTGTCCTTCCCCCACCTGTTGATCCAGGTTA  660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GTGTTTTTTTGTTTTTTTCCTAGAAATGTTTGTCCTTCCCCCACCTGTTGATCCAGGTTA  660

Query   661  AGGAATACTTTTTTACACTTTATTCAAA    688
             ||||||||||||||||||||||||||||
Sbjct   661  AGGAATACTTTTTTACACTTTATTCAAA    688
```

# Sequence 1336 matched with Sequence 447

```
Query=   Sequence ID 1336
Length=724


   SEQ ID NO: 447

ALIGNMENTS
 Identities = 724/724 (100%), Gaps = 0/724 (0%)

Query  1     CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTCTGTG   60

Query  61    AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTCGACATTCG   120

Query  121   GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTCCGTGCAGCACTA   180

Query  181   ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGGCAGCTGTGACTGTGTC   240

Query  241   AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTTCCACTGCCGTCTCCACAGGA   300

Query  301   AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCATCAAGGCATTTATTGCAGTGTACTA   360

Query  361   TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TTTGCTTCCAAAGGATCAGGCCCTGAGAACAATGACCTTATTTCCTACAACAGTGTCTGG   420

Query  421   GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GTTGCGTGCCAGCAGATGCCTCAGATACCAAGAGATAACAAAGCTGCAGCTCTTTTGATG   480
```

```
Query  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTGACCAAGAATGTGGATTTTGTGAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAA  540

Query  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCAC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAATGTGACCCTTACTCTGGCCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCAC  600

Query  601  AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AATCATGAGGATGATGTGTTGGGGTTTCCCAGCAATCAGGACTTGTATTGGTCAGAGGAC  660

Query  661  GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GATCAAGAGCTCATAATCCCATGCCTTGCGCTGGTGAGAGCATCCAAAGCCTGCCTGAAG  720

Query  721  AAAA  724
            ||||
Sbjct  721  AAAA  724
```

# Sequence 1337 matched with Sequence 448

Query=   Sequence ID 1337
Length=622


   SEQ ID NO: 448

ALIGNMENTS
 Identities = 622/622 (100%), Gaps = 0/622 (0%)

```
Query  1    CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAGAACTCTGGGACATTTGCAAAGGGTATGGCATATGTGTAATGGGAATACCAGAGGAG  60

Query  61   AGGAAAGACAGGAAGTCaaaaaaaGAATTTTTCCAAATTAATGATAGGTTCCAAACCACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGAAAGACAGGAAGTCAAAAAAAGAATTTTTCCAAATTAATGATAGGTTCCAAACCACA  120

Query  121  GATGCAGGAAGCTTAAACACCAACAGGATAAATAAAACAAAATCTACGCTTAAGCATATC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATGCAGGAAGCTTAAACACCAACAGGATAAATAAAACAAAATCTACGCTTAAGCATATC  180

Query  181  ATACTTAACCTGCAGAAAATTACAGACAAAGAAAAAACACCAGAGGGGAAGCTGGCAGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATACTTAACCTGCAGAAAATTACAGACAAAGAAAAAACACCAGAGGGGAAGCTGGCAGAA  240

Query  241  ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACATACCACCTATAGCGGAAGAAGAATAAGAATTACATCAGACTTCCCTTCAGAAATCTT  300

Query  301  GCAAACAAAAAGATGTAGCACAATATTTAAAGTATTAAAGGAGGCCGGGCCCGGTGGCTC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GCAAACAAAAAGATGTAGCACAATATTTAAAGTATTAAAGGAGGCCGGGCCCGGTGGCTC  360

Query  361  GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGCCTGTAATCCTAACACTTTGGGAGGCTGAGGCAGGAGGACCATGAGGTCAGGAGATC  420

Query  421  GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGACCATCCTGGTGATGGTGATACCCCATCTCTACTAAAAATACAAAAAATTAACCGGG  480
```

```
Query  481  CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATGGTGACACGCACCTGTAATCCCAGCTACTTGGGAGGCTGAAGCAGGAGAATCGTTTG  540

Query  541  AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AGCCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACATCACTGCACGCCTGGGCAACAG  600

Query  601  AGCGAGACTCCATCTCAAAAAA  622
            ||||||||||||||||||||||
Sbjct  601  AGCGAGACTCCATCTCAAAAAA  622
```

# Sequence 1338 matched with Sequence 449

Query=   Sequence ID 1338
Length=834


   SEQ ID NO: 449

ALIGNMENTS
 Identities = 834/834 (100%), Gaps = 0/834 (0%)

```
Query  1    CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGACCCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC  60

Query  61   TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTTTTTA  120

Query  121  AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAATCATTAGG  180

Query  181  GAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCAGCAGTGAGTTTA  240

Query  241  GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTAGTTGACTGGTGTTCAT  300

Query  301  ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGATATTTTTAAAAAACTGACCC  360

Query  361  TATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAACTCCTCGTA  420

Query  421  AGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAAGAATCATATTCCT  480
```

```
Query  481  TCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAATCTTCACTTCTTGAAGGA  540

Query  541  TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCATTCTCTGAGTAAATATTTATTG  600

Query  601  CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAAGAATGAAAGAGGAGGGAGAAT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CATGCTTATCTTGTATCAAGCATTGTGATGAAAGCACAAGAATGAAAGAGGAGGGAGAAT  660

Query  661  GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GTTTAGAGAATAAGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGA  720

Query  721  CAGGTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTTAACTATGTGCACATC  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  CAGGTTCAGGTTAGTAAGGGCGCTCATATTTTGACCCTGAATGTTAACTATGTGCACATC  780

Query  781  ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT   834
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  ATGCTAGCTATTCTAAATCAGGCATTTTCAAATGGAAGCAGGCACTGACATTTT   834
```

# Sequence 1344 matched with Sequence 450

Query=   Sequence ID 1344
Length=624


   SEQ ID NO: 450

ALIGNMENTS
 Identities = 624/624 (100%), Gaps = 0/624 (0%)

```
Query  1    CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGTGAAGGGTCTTTATGTATTAGTATTAGAGTGATCTTTTGATTATTTTCCTCACTATAA   60

Query  61   GGAAATTATTTCCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAAATTATTTCCTCAGGATGAGCTGCCATAACATTCCACTGTCTGATGGCAATTTTAAA   120

Query  121  GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCTGAAATTGAAGCCCATGGCTAGGCTATGAGAACCCTAGTTCGTATAGTAAAGTTGAT   180

Query  181  ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAAACTGCTGGAAACTGAAACTTA   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATCTTCTGGATGTATACTAATTTTAGGCTTTATTTTAAAACTGCTGGAAACTGAAACTTA   240

Query  241  GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACAAAAGTATTTTCAGGACATCATTTACAATGTTTAGCCCTAAAGAGTCAAGCTGTGGG   300

Query  301  ATTCTGAGTCTTTCATATGTTACAGCAGAAACTTAAAAGCAAGAGGAAATTGGCTGGGCA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTCTGAGTCTTTCATATGTTACAGCAGAAACTTAAAAGCAAGAGGAAATTGGCTGGGCA   360

Query  361  CAGTGGCTCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGGATCATGAGGTCAAGA   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAGTGGCTCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGTGGATCATGAGGTCAAGA   420

Query  421  GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GATTGAGACCATCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAATTA   480
```

```
Query   481   GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GCTGGGCGTGGTGGCACACGCCTGTAATCCCAGCTAGTCAGGAGGCTGAGGCAGGAGAAT   540

Query   541   ATCTTGAACTTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   ATCTTGAACTTGGGAGGCAGAGGTTGCAGTGAGCCAAGATTACATCACTGCACTCCAGCC   600

Query   601   TGGTGACAGAGCGAGACTCCGACT   624
              ||||||||||||||||||||||||
Sbjct   601   TGGTGACAGAGCGAGACTCCGACT   624
```

# Sequence 1348 matched with Sequence 451

Query=   Sequence ID 1348
Length=966


   SEQ ID NO: 451

ALIGNMENTS
 Identities = 966/966 (100%), Gaps = 0/966 (0%)

```
Query   1    CTGAAACTGCACTGAACCCACAGGTAGGTTACATCACAGGACAGAAATCTGAGGAGCTGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CTGAAACTGCACTGAACCCACAGGTAGGTTACATCACAGGACAGAAATCTGAGGAGCTGG   60

Query   61   AGAAAGCAAAAGAATAAAGGATGGGCTGACACCAGAAGGAATTAAAGGAATTTTTATACT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AGAAAGCAAAAGAATAAAGGATGGGCTGACACCAGAAGGAATTAAAGGAATTTTTATACT   120

Query   121  GAACTTCAATTACTTGTTCATTTGAAGTTTGtttttttAATGAACGTTTTTGCTGTTACT   180
             ||||||||||||||||||||||||||||||||       |||||||||||||||||||||
Sbjct   121  GAACTTCAATTACTTGTTCATTTGAAGTTTGTTTTTTTAATGAACGTTTTTGCTGTTACT   180

Query   181  TAAATATAGTGTTTTGAAAGTGTTTCAAATGTATTCAAGTTGGGATTTTCCATATTTTAC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TAAATATAGTGTTTTGAAAGTGTTTCAAATGTATTCAAGTTGGGATTTTCCATATTTTAC   240

Query   241  TACAGTTCTGTCTTAGTATGTTCACCATAAAACACTTATCATTAAAGCTCACAAAGTGCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TACAGTTCTGTCTTAGTATGTTCACCATAAAACACTTATCATTAAAGCTCACAAAGTGCT   300

Query   301  TTTTTGTAATATGAGGATAAAATGAAGCCATATAAGAAtttttttATATCTGTACATTTA   360
             ||||||||||||||||||||||||||||||||||||||       |||||||||||||||
Sbjct   301  TTTTTGTAATATGAGGATAAAATGAAGCCATATAAGAATTTTTTTATATCTGTACATTTA   360

Query   361  ACCCACATTTGAGCTTTAGCCAAAATATATAGCtttttttttttCTGACCTGGCCAACGTA   420
             |||||||||||||||||||||||||||||||||           |||||||||||||||||
Sbjct   361  ACCCACATTTGAGCTTTAGCCAAAATATATAGCTTTTTTTTTTCTGACCTGGCCAACGTA   420

Query   421  TTATCCAGCAAACATCAACTGAAGCAATATGGAAACACTTCCAAATGTTTGCCAATAATG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TTATCCAGCAAACATCAACTGAAGCAATATGGAAACACTTCCAAATGTTTGCCAATAATG   480
```

```
Query  481  CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACTAAAGAGGCATTATACATTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTATTAAGTGACTGATGTCAACATTAGTTACATGGCAAACTAAAGAGGCATTATACATTT  540

Query  541  TTAAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTCAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TTAAAACACACTAACATATAACTGTAGATAATGTAAGGTTTATTTATATGCATATTTCAT  600

Query  601  AGtatatttaaatgtttaaatataaaaaagggtttttaaacacttttaattttttatcttt  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AGTATATTTAAATGTTTAAATATAAAAAAGGGTTTTTAAACACTTTTAATTTTTATCTTT  660

Query  661  gattttttttATTGATATCTCTTTCCAGGCTACTAATAAAATTGCCAGAACTAAACTATC  720
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GATTTTTTTTATTGATATCTCTTTCCAGGCTACTAATAAAATTGCCAGAACTAAACTATC  720

Query  721  AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTCGTTTTGAATTACAAT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  AGGTAAAGGTTAAGGCATCAATTGACAAGTAAGTTTTCTAATTTCGTTTTGAATTACAAT  780

Query  781  TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  TCCAAATGTAAGACTTTTAAAAATGAATGGCCTTTATTTTATAGAATAATTTTGACCTTT  840

Query  841  TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA  900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841  TAAATTTACTTATCTAACATTATATAATGAATGTACTTCAAATATTTGACTTTGAAGTCA  900

Query  901  ACATTAACAAATTCATGGATCCTAATTAAAATTTACTATAAAACTGGAATCATTTATTAC  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901  ACATTAACAAATTCATGGATCCTAATTAAAATTTACTATAAAACTGGAATCATTTATTAC  960

Query  961  TTCCTT   966
            ||||||
Sbjct  961  TTCCTT   966
```

# Sequence 1351 matched with Sequence 452

Query=   Sequence ID 1351
Length=725


   SEQ ID NO: 452

ALIGNMENTS
 Identities = 725/725 (100%), Gaps = 0/725 (0%)

```
Query  1    tttttttttttttAAAAGAGATGGGTTCTCACTATGTTGCCCATAATGTTTATGAGATTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTTTTTTTTTTAAAAGAGATGGGTTCTCACTATGTTGCCCATAATGTTTATGAGATTA  60

Query  61   AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATACCACCATTTATTTATC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGTTCATCTTTTTTATCTGAGTAGTATTTTATTGTATGAATATACCACCATTTATTTATC  120

Query  121  TGTTGGTTATTTCCAGTTTTGGGCTATAATCCAAAATGCTTTTTTCAAACAATAGGCTAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGTTGGTTATTTCCAGTTTTGGGCTATAATCCAAAATGCTTTTTTCAAACAATAGGCTAT  180

Query  181  ATATCATTAATGTCCGTTTATCAGCAGtataaaatatcttaccataaatattaataaaag  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATATCATTAATGTCCGTTTATCAGCAGTATAAAATATCTTACCATAAATATTAATAAAAG  240

Query  241  aagcattcatatataaaatatagatatTTCAAACCCTACAGAGGGCCTTTTAATGATTAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGCATTCATATATAAAATATAGATATTTCAAACCCTACAGAGGGCCTTTTAATGATTAA  300

Query  301  ATATTTTGTCCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTTAACCTGCCTTAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATATTTTGTCCTTACAAAAAGGTCCAGGTAATTACACCCATGAGGTTAACCTGCCTTAGT  360

Query  361  GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCAGGACTTAAAATAAGGCTTCTCCTGCCATCTCTCTCCATTTGTAGAATGTGAAATTCT  420

Query  421  TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTTTGTTCTCTTCTTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTAAAATGCATCCTATATTAGGAATACTATAGCTGTGCACTGGTGTTTGTTCTCTTCTTT  480
```

```
Query  481  AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAACTCGGGACCGTATATATCTGCTCAAATTGCCCAAGTATACATATGCTGCACTCCATC  540

Query  541  AAGTGTGTCAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAGTGTGTCAGGCCACATTCTATCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGA  600

Query  601  GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GCTCTATTTGGATCCCTCTTACCCTACCTTTTATATTTATGACAGCATTATCATAAAACT  660

Query  661  CCAATATTCTTCAATAACTTACATGTTTGTTGTAGGATAAAATTATTACCCTCAATGAAC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CCAATATTCTTCAATAACTTACATGTTTGTTGTAGGATAAAATTATTACCCTCAATGAAC  720

Query  721  TACAT  725
            |||||
Sbjct  721  TACAT  725
```

# Sequence 1352 matched with Sequence 453

Query=   Sequence ID 1352
Length=715


    SEQ ID NO: 453

ALIGNMENTS
 Identities = 715/715 (100%), Gaps = 0/715 (0%)

```
Query  1    ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTTGCTAACACATCAAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACCAGCTTCTTCACAGGTTCCACGAGTCATGTCAACACAGCGTGTTGCTAACACATCAAC  60

Query  61   ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACAGACAATGGGTCCACGTCCTGCAGCTGCAGCCGCTGCAGCTACTCCTGCTGTCCGCAC  120

Query  121  CGTTCCACAGTATAAATATGCTGCAGGAGTTCGCAATCCTCAGCAACATCTTAATGCACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGTTCCACAGTATAAATATGCTGCAGGAGTTCGCAATCCTCAGCAACATCTTAATGCACA  180

Query  181  GCCACAAGTTACAATGCAACAGCCTGCTGTTCATGTACAAGGTCAGGAACCTTTGACTGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCCACAAGTTACAATGCAACAGCCTGCTGTTCATGTACAAGGTCAGGAACCTTTGACTGC  240

Query  241  TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCCATGTTGGCATCTGCCCCTCCTCAAGAGCAAAAGCAAATGTTGGGTGAACGGCTGTT  300

Query  301  TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCTCTTATTCAAGCCATGCACCCTACTCTTGCTGGTAAAATCACTGGCATGTTGTTGGA  360

Query  361  GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATTGATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGT  420

Query  421  TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGCAGT  480
```

```
Query  481   TAACAGTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAAACTT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TAACAGTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAAGAAACTT   540

Query  541   GTGCTTCACCGAAGaaaaatatctaaacatcgaaaaacttaaatattatggaaaaaaaac   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GTGCTTCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTATGGAAAAAAAAC   600

Query  601   attgcaaaatataaaataaataaaaaaaggaaaggaaaCTTTGAACCTTATGTACCGAGC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ATTGCAAAATATAAAATAAATAAAAAAAGGAAAGGAAACTTTGAACCTTATGTACCGAGC   660

Query  661   AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTTAAAA    715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   AAATGCCAGGTCTAGCAAACATAATGCTAGTCCTAGATTACTTATTGATTTAAAA    715
```

# Sequence 1353 matched with Sequence 454

Query=   Sequence ID 1353
Length=573


   SEQ ID NO: 454

ALIGNMENTS
 Identities = 573/573 (100%), Gaps = 0/573 (0%)

```
Query  1    ACATTCTGGAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACATTCTGGAAAAGGCAAAAGGGAGGAAGAACTGATTAGTGGTTAGCCCAGGGTTAGAGT  60

Query  61   TGGGGAGAGGATATAATGAGGGAACTTTTGTGGATTCTGTACCATGATTATGATTACACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGGGGAGAGGATATAATGAGGGAACTTTTGTGGATTCTGTACCATGATTATGATTACACA  120

Query  121  AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AACCTATGCATACATTGAAACACATAGAACTATACGTTGAAAAAAGTGAATCTGCCTGTA  180

Query  181  TGTaaatttaaaagaaaaatattttttaaaaaaaCAGATGCTTCTTAACACATTATCAT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGTAAATTTAAAAGAAAAATATTTTTTTAAAAAAACAGATGCTTCTTAACACATTATCAT  240

Query  241  CTATGTCAGTTTAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTATGTCAGTTTAACAGTTAGTAGACTTAGGCCAGGTGTCATGGCTCACTCCTGTAATCC  300

Query  301  CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGTGCTTTGGGAGTCTGAGGTGGGACGATCTCTTGAGACTAGGAGGGAGTTTGAGACAA  360

Query  361  ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACCTAGGCAATGTAATGAGACTCTTTCTCTACAAAAAATTTTAAAGTTATCTGGACATGG  420

Query  421  TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGGTGCCTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTCCTTGAGCCC  480
```

```
Query  481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGAAGTTCAAGGCTACAGTGTGCTATGATAGAGCCACTGCACTCCAGCCTGGGCAACCAG  540

Query  541  GTGAGACCTTGTCTCTAAAATGAATAAATAAAT  573
            |||||||||||||||||||||||||||||||||
Sbjct  541  GTGAGACCTTGTCTCTAAAATGAATAAATAAAT  573
```

# Sequence 1355 matched with Sequence 455

Query= Sequence ID 1355
Length=498


   SEQ ID NO: 455

ALIGNMENTS
 Identities = 498/498 (100%), Gaps = 0/498 (0%)

```
Query  1    TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGGTCTTTCACCCAGCCAGGGAGAAGGTTCTTCGCTCAGTATGAAGAAAAGCAACCCAAA  60

Query  61   ACTCTCAATCTGATTTGTTTTTGTTTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTCTCAATCTGATTTGTTTTTGTTTATGTCGATGCCCTGTAGTTTGAAAGTGAAGTAAA  120

Query  121  GATTTAGAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTaaaa  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATTTAGAATTCACCTAAGTCCAAAGGAAAACACGTGGTTTTTAAAGCCATTAGGTAAAA  180

Query  181  aaaGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAAGTTCTCAATAAAGGCATTACAATTTTTTAGGTTTAGAAAGATGGACTTTTCTGATAA  240

Query  241  ATCTTGGCAGACATCTaaaaaaaaaaaCCATATTTTTCACAAGAAAATGCAAGTTACtttt  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATCTTGGCAGACATCTAAAAAAAAAAACCATATTTTTCACAAGAAAATGCAAGTTACTTTT  300

Query  301  tttGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTGGAAATAATACTCACTGATTATGGATAAAATGGAATATTTTCAGATACTATATTGGC  360

Query  361  TGTTTCAAAATAGTACTATTCTTTAAACTTGTAATTTTTGCTAAGTTATTTGTCTTTGTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGTTTCAAAATAGTACTATTCTTTAAACTTGTAATTTTTGCTAAGTTATTTGTCTTTGTT  420

Query  421  GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTATCTATAAATATGTAAAAAATATTTAAATAGATGTACCTGTTTTGCTTTCACACTTAA  480
```

```
Query   481   TAAAAAAttttttttttGT   498
              ||||||||||||||||||
Sbjct   481   TAAAAAATTTTTTTTTGT   498
```

# Sequence 1359 matched with Sequence 456

Query=   Sequence ID 1359
Length=732


   SEQ ID NO: 456

ALIGNMENTS
 Identities = 732/732 (100%), Gaps = 0/732 (0%)

```
Query  1    CGGGATCCCTAGTATAACACATTCAGTGTTCCCCTTTCAGTCTTACTACTTTGACCGCGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGGGATCCCTAGTATAACACATTCAGTGTTCCCCTTTCAGTCTTACTACTTTGACCGCGA  60

Query  61   TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGATGTGGCTTTGAAGAACTTTGCCAAATACTTTCTTCACCAATCTCATGAGGAGAGGGA  120

Query  121  ACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATGCTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGA  180

Query  181  TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATT  240

Query  241  ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACATTTGGAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCACTGACAAA  300

Query  301  AATGACCCCCATGTGAGTATTGGAACCCCAGGAAATAAATGGAGGAAATCATTTGCCTTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATGACCCCCATGTGAGTATTGGAACCCCAGGAAATAAATGGAGGAAATCATTTGCCTTA  360

Query  361  GGGATTGGGAAAGCTGCCCACTAACTGTCTTCCCCATTGTTTTGCAGTTGTGTGACTTCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGATTGGGAAAGCTGCCCACTAACTGTCTTCCCCATTGTTTTGCAGTTGTGTGACTTCA  420

Query  421  TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTGAGACACATTACCTGAATGAGCAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGA  480
```

```
Query  481  CCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCAACTTGCGCAAGATGGGAGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGC  540

Query  541  ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACACCCTGGGAGACAGTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTG  600

Query  601  GGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGGTGACTTCCCTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCT  660

Query  661  ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTACCATTCCTTCAAATAAAG  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  ATAAGTTGTACCAAAACATCCACTTAAGTTCTTTGATTTGTACCATTCCTTCAAATAAAG  720

Query  721  AAATTTGGTACC  732
            ||||||||||||
Sbjct  721  AAATTTGGTACC  732
```

# Sequence 1360 matched with Sequence 457

Query=   Sequence ID 1360
Length=465


   SEQ ID NO: 457

ALIGNMENTS
 Identities = 465/465 (100%), Gaps = 0/465 (0%)

```
Query  1    TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGCGCAGACCAGACTTCGCTCGTACTCGTGCGCCTCGCTTCGCTTTTCCTCCGCAACCAT  60

Query  61   GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACTGAAGAAGAC  120

Query  121  AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAACAGGAGAAGCAAGC  180

Query  181  AGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTACATTCCACAAGCATTGCC  240

Query  241  TTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTCTTATTTTACTTCTTTTAGCTGTTTAACTTTGTAAGATGCAAAGAGGTTGGATCAAGT  300

Query  301  TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTAAATGACTGTGCTGCCCCTTTCACATCAAAGAACTACTGACAACGAAGGCCGCGCCTG  360

Query  361  CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCTTTCCCATCTGTCTATCTATCTGGCTGGCAGGGAAGGAAAGAACTTGCATGTTGGTGA  420

Query  421  AGGAAGAAGTGGGGTGGAAGAAGTGGGGTGGGACGACAGTGAAAT     465
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGGAAGAAGTGGGGTGGAAGAAGTGGGGTGGGACGACAGTGAAAT     465
```

# Sequence 1361 matched with Sequence 458

Query=   Sequence ID 1361
Length=788


   SEQ ID NO: 458

ALIGNMENTS
 Identities = 788/788 (100%), Gaps = 0/788 (0%)

```
Query  1    TATAAATACACTCCGGGATGATTTACCCCCGGAGGTCAGCTAGTAAAATACATGAGTAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TATAAATACACTCCGGGATGATTTACCCCCGGAGGTCAGCTAGTAAAATACATGAGTAGA  60

Query  61   ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAATCATAAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATTCCTTAAAGTATGTGATAATTGCTCATCACTATCCAAGTGTGACATAAATCATAAAAA  120

Query  121  GAATTGACAAAATCAGGGTCGCAAAGAGAATTGaaaaaaaTCTGTCACAACCAAAATTTA  180
            |||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Sbjct  121  GAATTGACAAAATCAGGGTCGCAAAGAGAATTGAAAAAAAATCTGTCACAACCAAAATTTA  180

Query  181  AATTGACCTCTGTCCTAGAGTATGAGAGCCACACTGAACAGAAAAACCAGATAAATCTTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATTGACCTCTGTCCTAGAGTATGAGAGCCACACTGAACAGAAAAACCAGATAAATCTTT  240

Query  241  TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTCACCCCACCTCCCCATGTCCT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TATAAAATATTCATTTGCAGCCCCATTAACGTTGCTTGTCACCCCACCTCCCCATGTCCT  300

Query  301  TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGACAAACTGAATGTATAGTAACATCATCCCAGGCCAGGCGCGGTGGCTCATGCCTGTA  360

Query  361  ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATCCCAGCACTTTGTGAGGCTAAGGCAGGCAGATCAGGAGGTCAGGAGTTCAGGACCAGC  420

Query  421  CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTGGCCAAAAAGGTGAAACTCCGTCTCTACTAACAATACAAAAATTAGCTGGGTGCGGTA  480
```

```
Query   481   GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GTAGGCGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTCAAACCCGG   540

Query   541   AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   AAGGTGGAGGTTGCAGTGAGCTGAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGC   600

Query   601   AAGACTCTGTCTCGGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT   660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   AAGACTCTGTCTCGGGGAGGGGGGTGGCGGAGATAAAGAAATAACATCATCTTATACTGT   660

Query   661   CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTTCTCAGGGAAGAT   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   CAAGCTCAAGGTGTCTGCAGCCTTATCTTCAGGGGAAGTTGTGTCTTTCTCAGGGAAGAT   720

Query   721   ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTCAGAGAGGAAAATGCAGTAG   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721   ACAGATTTCAATTTAGAGCAAGACAGAGAGAAGTTACATTCAGAGAGGAAAATGCAGTAG   780

Query   781   TCTAACTG   788
              ||||||||
Sbjct   781   TCTAACTG   788
```

# Sequence 1364 matched with Sequence 459

Query=   Sequence ID 1364
Length=423


    SEQ ID NO: 459

ALIGNMENTS
 Identities = 423/423 (100%), Gaps = 0/423 (0%)

```
Query  1     GCGGCCGCGCTCTTTTCAATTTTTAAAAAGAAGTTTGTTTTCCATTTCAGTAATTTCTGC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCGGCCGCGCTCTTTTCAATTTTTAAAAAGAAGTTTGTTTTCCATTTCAGTAATTTCTGC   60

Query  61    TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTTGCCTTTTCT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTTGATCTTCCTTATGTCCTCCTATTGAGTTGATCAGCTTTCTTTATTCTTGCCTTTTCT   120

Query  121   CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAATGGCTGATGCC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCTCTGTGTGCCCTTTCTATTAACGTATTTACCCTTAGGCTGGGCACAATGGCTGATGCC   180

Query  181   TGTAATCCCTGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGTAATCCCTGCACTTTGGGAGGCCGAGGCAGGTGGATCACCTAAGGTCAGGAGTTCAAG   240

Query  241   ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ACCAGCCTGGCCAACATGGTGAAACCTGGTCTCTACTAAAAACACAAAAATTAGCCAGGC   300

Query  301   ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ATGGTGGTGTGCACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGA   360

Query  361   ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAATGAGACTTTGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ACCTGGGAGGCGGAGATTGTGCCAAAGCACTCCAGCCTGGGCAACAAAATGAGACTTTGT   420

Query  421   GTC   423
             |||
Sbjct  421   GTC   423
```

# Sequence 1365 matched with Sequence 460

```
Query=   Sequence ID 1365
Length=231


   SEQ ID NO: 460

ALIGNMENTS
 Identities = 231/231 (100%), Gaps = 0/231 (0%)

Query  1    CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CACCAGGCTGTCTTCAGATACTTCATACAGAAATGAGCCTCCCTGTGGGGTCCTCTTCCC  60

Query  61   TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCCTTCAGCCTGTCCATCAACACAGCATTGCGGGATCCTTACCATGGCATCCAGCCCTGG  120

Query  121  AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATGCTTCAGGAAAGTTGCAGGTCCATGCTGCAGGACAGGCTCAGATCAGCAGAGACGC  180

Query  181  ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA  231
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATCTCACATCGGGCTGTGAAATTCAAGTTGAGCTGCAATTGGCAATGAGAA  231
```

# Sequence 1366 matched with Sequence 461

Query= Sequence ID 1366
Length=687


   SEQ ID NO: 461

ALIGNMENTS
 Identities = 687/687 (100%), Gaps = 0/687 (0%)

```
Query  1    GTTATTCACTGAGACCGTGCCCCGGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTTATTCACTGAGACCGTGCCCCGGTTATGAGGTTGTACCAGAAAGCAAGTATTCACTAT  60

Query  61   GCACACTATTCACCGCTCACCCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCACACTATTCACCGCTCACCCTAGCATTGAAGCCAGCCTGTAGCCTGAAAGCCTTTGCT  120

Query  121  TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTGAGGGCAGGTCTTTCCCCAAAATGCAGACACGAAGGTGCAAAGTGAAGCTGCCAGTCT  180

Query  181  TGCAAAAGATGTAACTTGTCACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCCACATTTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCAAAAGATGTAACTTGTCACGAAGGCCACGAGTGGCAGGGAGAGCTGTCCCACATTTG  240

Query  241  CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGGAAGTGGCTATGTGAGGACGGGGGAGGCGGGTCCCTTAGAGATGAGACAATCATAAGG  300

Query  301  GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGAGATATCAGAGAAAATCGTAAGGGGAGCAGATGGTTGTCAAGAGAATAGGCTGACCAT  360

Query  361  CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CGAAGGACTGGCAGAAGCTTTCAGAAAACCACTGGACGGCTGGGCACAGTGGCTTAGGCC  420

Query  421  TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGTAATCCCAGCACTTTGGGAGGCTGACGCAGGTGAATCACTTGAGGTCAGGAGTTCCAG  480
```

```
Query  481  ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAATTAGCCAGGC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACCAGCCTGGCCAACATGGTGAAACCCCATCTCTACAGAAAATATAAAAATTAGCCAGGC  540

Query  541  GTGGTGGCACAAGCCTAGAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTGGTGGCACAAGCCTAGAATCCCAGCTACTTGGGAGGCTGAGGCAGGCGAATGGCTTGA  600

Query  601  ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACCCAGGAGTCAGAGGCTGCAGTGAGTCGAGATTGTTCCACTGCACTCCAGCCTGGGTGA  660

Query  661  CAGTGCAAGACTCCTTCCaaaaaaaaa  687
            |||||||||||||||||||||||||||
Sbjct  661  CAGTGCAAGACTCCTTCCAAAAAAAAA  687
```

# Sequence 1367 matched with Sequence 462

Query=   Sequence ID 1367
Length=874


   SEQ ID NO: 462

ALIGNMENTS
 Identities = 874/874 (100%), Gaps = 0/874 (0%)

```
Query  1    TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTCGTGAGTGATGGCGTCCCGGGTTGCTTGCCGGTGCTGGCCGCCGCCGGGAGAGCCCGG  60

Query  61   GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCTG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCAGAGCAGAGGTGCTCATCAGCACTGTAGGCCCGGAAGATTGTGTGGTCCCGTTCCTG  120

Query  121  ACCCGGCCTAAGGTCCCTGTCTTGCAGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCCGGCCTAAGGTCCCTGTCTTGCAGCTGGATAGCGGCAACTACCTCTTCTCCACTAGT  180

Query  181  GCAATCTGCCGATAtttttttttGTTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCAATCTGCCGATATTTTTTTTTGTTATCTGGCTGGGAGCAAGATGACCTCACTAACCAG  240

Query  241  TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGCTGGAATGGGAAGCGACAGAGCTGCAGCCAGCTTTGTCTGCTGCCCTGTACTATTTA  300

Query  301  GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGGTTCAGTGCGGAGAGCCCTGACTCAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTGGTCCAAGGCAAGAAGGGGGAAGATGTTCTTGGTTCAGTGCGGAGAGCCCTGACTCAC  360

Query  361  ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTGACCACAGCTTGAGTCGTCAGAACTGTCCTTTCCTGGCTGGGGAGACAGAATCTCTA  420

Query  421  GCCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GCCGACATTGTTTTGTGGGGAGCCCTATACCCATTACTGCAAGATCCCGCCTACCTCCCT  480
```

```
Query  481  GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAGGAGCTGAGTGCCCTGCACAGCTGGTTCCAGACACTGAGTACCCAGGAACCATGTCAG  540

Query  541  CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CGAGCTGCAGAGACTGTACTGAAACAGCAAGGTGTCCTGGCTCTCCGGCCTTACCTCCAA  600

Query  601  AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAGCAGCCCCAGCCCAGCCCCGCTGAGGGAAGGGCTGTCACCAATGAGCCTGAGGAGGAG  660

Query  661  GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GAGCTGGCTACCCTATCTGAGGAGGAGATTGCTATGGCTGTTACTGCTTGGGAGAANGGC  720

Query  721  CTAGAAAGTTTTGCCCCCGCTGCGGCCCCAGCANAATCCAGTGTTGCCTGTGGCTGGAGA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  CTAGAAAGTTTTGCCCCCGCTGCGGCCCCAGCANAATCCAGTGTTGCCTGTGGCTGGAGA  780

Query  781  AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCCACCTTGGGAA  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  AAGGAATGTGCTCATCACCAGTGCCCTCCNTTACGTCAACAATGTCCCCCACCTTGGGAA  840

Query  841  CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT      874
            |||||||||||||||||||||||||||||||||||
Sbjct  841  CATCATTGGTTGTGTGCTCAGTGCCCGATGTCTT      874
```

# Sequence 1368 matched with Sequence 463

Query=   Sequence ID 1368
Length=585


   SEQ ID NO: 463

ALIGNMENTS
 Identities = 585/585 (100%), Gaps = 0/585 (0%)

```
Query  1    CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGTGAGCCAAGATCACACCACTGCACTCCAGCCTGGACAACAGAACGAGACTCCATATC  60

Query  61   aaaaaaattaaattaaaatataataaaatTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAAAAAATTAAATTAAAATATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACCTGTAA  120

Query  121  TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGACCATCC  180

Query  181  TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGGCTAATACAGTGAAACCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGCATGGTG  240

Query  241  GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGAACCCGG  300

Query  301  GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAGCAGAAC  360

Query  361  GAGACTCCATCTCaaataaaataaataaataaaatGAATTTCAGCTAGAAGAGCCTTATTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGACTCCATCTCAAATAAATAAATAAATAAAATGAATTTCAGCTAGAAGAGCCTTATTC  420

Query  421  CATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTATCATATA  480
```

```
Query  481  TTCTTATGCGAATTATTATTTTCGCCttttttttttATAATTCTGTCTGGGATTTGAATAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTCTTATGCGAATTATTATTTTCGCCTTTTTTTTTATAATTCTGTCTGGGATTTGAATAG  540

Query  541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAAT  585
```

# Sequence 1369 matched with Sequence 464

```
Query=   Sequence ID 1369
Length=305


   SEQ ID NO: 464

ALIGNMENTS
 Identities = 305/305 (100%), Gaps = 0/305 (0%)

Query  1    CTGATTGCAAAAACATTACAACTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGATTGCAAAAACATTACAACTCAGTACTGCGGCTTTCATTCAAATAGGTTATATGTAT   60

Query  61   AAACTGAGGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAACTGAGGTTCAACAATATTGTATTTGAGATGGGAAAGTTAAAGAAATGCAATAATGTA   120

Query  121  AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AATAATACTTAAGAAAATAAGATCTCAGGAAACTGTGTATACTCTGTACTTTTATGCAAC   180

Query  181  TTTATCAGATCATTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACTTTGAG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTATCAGATCATTTCAGTATATGCATCAAGGATATAGTGTATATGACATGAACTTTGAG   240

Query  241  TGCAAAAACTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGttt   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCAAAAACTGTACTATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGTTT   300

Query  301  ttttG   305
            |||||
Sbjct  301  TTTTG   305
```

# Sequence 1370 matched with Sequence 465

Query= Sequence ID 1370
Length=422


   SEQ ID NO: 465

ALIGNMENTS
 Identities = 422/422 (100%), Gaps = 0/422 (0%)

```
Query  1    CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAATGCTTTTAGATTAAAA  60

Query  61   TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAGTTGTAGGTGATTAAAATAATTT  120

Query  121  GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAAGGCGATCTTTTAAAAAGAGATTAAACCGAAGGTGATTAAAAGACCTTGAAATCCATG  180

Query  181  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACGCAGGGAGAATTGCGTCATTTAAAGCCTAGTTAACGCATTTACTAAACGCAGACGAAA  240

Query  241  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGGAAAGATTAATTGGGAGTGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTTGAAG  300

Query  301  TGGAAAACTGGAAGACAGAAGTACGGGAAGGCgaagaaaagaatagataagatagggaaa  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGGAAAACTGGAAGACAGAAGTACGGGAAGGCGAAGAAAAGAATAGATAAGATAGGGAAA  360

Query  361  ttagaagataaaaacatacttttagaagaaaaaagataaaTTTAAACCTGAAAAGTAGGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTAGAAGATAAAAACATACTTTTAGAAGAAAAAAGATAAATTTAAACCTGAAAAGTAGGA  420

Query  421  AG  422
            ||
Sbjct  421  AG  422
```

## Sequence 1371 matched with Sequence 466

Query=   Sequence ID 1371
Length=833


   SEQ ID NO: 466

ALIGNMENTS
 Identities = 833/833 (100%), Gaps = 0/833 (0%)

```
Query  1    GTCCAGNAGAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTCCAGNAGAAAGTTCAGTGACTTGTCCAGAGCTGCAGGTCTTAAGAGGCTGAAATCTCG  60

Query  61   CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTCTGCCTCGAGGCTGCGGTTCCACTGACCCATACTACTTGCCTTCAGGAAAGAGAAAT  120

Query  121  GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GGTGTAGGAAGGCTGTGGATGAAGACGCTTACATTCATGAAGGATTTGGATAGGCGAACA  180

Query  181  TGAGCTTTTCCACCAAATTTCAGAATTTTAAGAAATGCCTTAAATTATTTCTTAAAAATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGCTTTTCCACCAAATTTCAGAATTTTAAGAAATGCCTTAAATTATTTCTTAAAAATC  240

Query  241  AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTTAGGGAACATGATAAAATTCTGAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTTGGGGCAGACGAGAAGTTCTGATAATAGTTTTTAGGGAACATGATAAAATTCTGAC  300

Query  301  CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTAGAAGTGGTATACCAGTTTGAGAAGAAGAACAAGCTATAAACGGTGTAGATAACATT  360

Query  361  CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CACGGCTATTTAAGAAAGAGTTACTAAGGGAAACCAGAATGACTTAAGAGTGTTACTCTT  420

Query  421  CTTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CTTTTTCTGAGAGAACAATAGCATCATCTCAGAAAGCCTTTCATGCCATTAATAGGTAAG  480
```

```
Query  481   AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTCCT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AATCTGGGCTTCTTGGACCATGGGTTAGACTTTCTTACAAAACCATAATATGCATTTCCT   540

Query  541   AGCAAAATTTATGCTATTACATTTCCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGCAAAATTTATGCTATTACATTTCCTTATCTCAACAAAGACTGGTAAATTCAGTACTTA   600

Query  601   TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TTCCTCAATTTTCCTACCCTTAAAATGGGGATATTCTGCCTCTCCAAGGAATGCTGGGAA   660

Query  661   CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTCATGGAAGTTTAGGTTATTTATATG   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CAAGCAAGTCCTCATGTTAGGGGTCTTTGAGTTTTCATGGAAGTTTAGGTTATTTATATG   720

Query  721   ATGACATAGTTGTCAACTTACTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   ATGACATAGTTGTCAACTTACTTTCAGGATGGACTTTTCTTTTGTGAGTTTGTGACCTAA   780

Query  781   ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG   833
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   ATACAATAGTTGTTATGCATGTCCAGTTTATGGAAGTACCACTGCAATANCAG   833
```

# Sequence 1372 matched with Sequence 467

```
Query=   Sequence ID 1372
Length=594


   SEQ ID NO: 467

ALIGNMENTS
 Identities = 594/594 (100%), Gaps = 0/594 (0%)

Query  1    CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGTGCAGCCAAGTATCACACCACTGCACTCCAGTCCTGGACAACAGAAACGANTACTCC  60

Query  61   ATATCaaaaaaaTTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATATCAAAAAAATTAAATTAAANGATAATAAATTTCTTGCCGGGCGCAGTGGCTCACACC  120

Query  121  TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAAGTCAGGAGATTGAGAC  180

Query  181  CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CATCCTGGCTAATACAGTGAAATCCCCGTCTCTACTATAAATACAAAAAATTAGCTGGGC  240

Query  241  ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGGTGGCGGGCGTCTGTAGTCCCAGCTACTCAGGAGTCTGAGGCAGGAGAATGGTGTGA  300

Query  301  ACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCAATCCAGCCTGGGCAG  360

Query  361  CAGAACGAGACTCCATCTCaaataaataaataaataaaatGAATTTCAGCTAGAAGAGCC  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAGAACGAGACTCCATCTCAAATAAATAAATAAATAAAATGAATTTCAGCTAGAAGAGCC  420

Query  421  TTATTCCATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTATTCCATTTTCCTTTTTATTAAACATCTGGCATAAGTTGGTAAGTATGTGAAGTTTAT  480
```

```
Query  481  CATATATTCTTATGCGAATTATTATTTTCGCCttttttttttATAATTCTGTCTGGGATTT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CATATATTCTTATGCGAATTATTATTTTCGCCTTTTTTTTTATAATTCTGTCTGGGATTT  540

Query  541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GAATAGTAGAGTTTGAATTCAGGAAGGACACCTGTGATAGGACAATAAAATCTA  594
```

# Sequence 1374 matched with Sequence 468

Query= Sequence ID 1374
Length=112


   SEQ ID NO: 468

ALIGNMENTS
 Identities = 112/112 (100%), Gaps = 0/112 (0%)

```
Query  1    GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTTGTTTGCCATCTGAGTCTT   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GAAAGCACATATGATATACATGTGTGTCATATGTATTATTTTGTTTGCCATCTGAGTCTT   60

Query  61   CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT  112
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CAAAATTTGTTACAGAATACCTGCATATTAATATTTCAAGGTATGGATTAAT  112
```

# Sequence 1378 matched with Sequence 469

BLASTN 2.2.22+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

Query=   Sequence ID 1378
Length=40

   SEQ ID NO: 469                                    79.8    1e-21

ALIGNMENTS
 Identities = 40/40 (100%), Gaps = 0/40 (0%)

```
Query  1    CTGAGTATTAACTAAAAAAAAAAAAAAAAAAAAAAAAAAAA  40
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGAGTATTAACTAAAAAAAAAAAAAAAAAAAAAAAAAAAA  40
```

# Sequence 1380 matched with Sequence 470

Query=   Sequence ID 1380
Length=933


    SEQ ID NO: 470

ALIGNMENTS
 Identities = 933/933 (100%), Gaps = 0/933 (0%)

```
Query  1    CCAAACCCAACTGGTCCAGTAGGATACTCACCTTACAGGGGGCGTCTCAAGAGTCTCACA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCAAACCCAACTGGTCCAGTAGGATACTCACCTTACAGGGGGCGTCTCAAGAGTCTCACA   60

Query  61   GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTTCCCTTGGGTCTTAAGAGACTCACTGTTGGACCAGGCGTGGTGACTCACGCCTGTAAA   120

Query  121  ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCAGCACTTTGGGAGGCCGAGGCGGGCGGATCAGTTGAGGTCAAGAGTTCAAGACCAGC   180

Query  181  CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGACCAAGGTGCTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTG   240

Query  241  GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTGTGCGCCTGTAATCCCAGCTACTCCAGAGGCTGAGGCAGGAGAATCTCTTGAACCCAG   300

Query  301  GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAGGTGGAGGTTGCAGTGAGTCGAGATCATGCCACTGCACTCCAGCCTGGGTGACAGAGC   360

Query  361  GAGACTCCGTCTTAGaaaaaaaaaaaaaaaaaaaaaaGAACCTCACAGTTCAGCAGGGTTC   420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GAGACTCCGTCTTAGAAAAAAAAAAAAAAAAAAAAAAGAACCTCACAGTTCAGCAGGGTTC   420

Query  421  TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGGAAAGAGTGAGAACAGGTCAA   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAGCATGAGACAATGAGGACAAGGGTAGGTGAGCAGGTGGAAAGAGTGAGAACAGGTCAA   480
```

```
Query  481   TTGTGATGGAGAAAATAATAAAGACAGAAAAGGCAGAAGACTGCCTGGCAGAAGACCTGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TTGTGATGGAGAAAATAATAAAGACAGAAAAGGCAGAAGACTGCCTGGCAGAAGACCTGT   540

Query  541   CCCAGCAGATACAAAAATACAGACAACAGGAGCCAGCATAGACCCTTGACCTGTGTAAGT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CCCAGCAGATACAAAAATACAGACAACAGGAGCCAGCATAGACCCTTGACCTGTGTAAGT   600

Query  601   CTTTCTCAGGCCTTCTTTTAAGTAGAAACATGCCTTTGaaaaaaaGTTTTAATAAACAGG   660
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  601   CTTTCTCAGGCCTTCTTTTAAGTAGAAACATGCCTTTGAAAAAAAGTTTTAATAAACAGG   660

Query  661   AAAATCATAAATCCCTATTTACATAAATAATATATCCTGGTCTTATTCTTAAAACCATTG   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   AAAATCATAAATCCCTATTTACATAAATAATATATCCTGGTCTTATTCTTAAAACCATTG   720

Query  721   ATTTTTCACGGCTCATTAANAAAGCTGGGCGAGGTGGCTCACGCCCGTCATCCTAGCACT   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   ATTTTTCACGGCTCATTAANAAAGCTGGGCGAGGTGGCTCACGCCCGTCATCCTAGCACT   780

Query  781   TTGGGAGGCCGAGGCGGGCANATCACAAGGTGAGGAGTTGGGAGACCAGCCTGACCAACA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   TTGGGAGGCCGAGGCGGGCANATCACAAGGTGAGGAGTTGGGAGACCAGCCTGACCAACA   840

Query  841   CGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTANCTGGGGGTGGTGGTGTGTGCCT   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   CGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTANCTGGGGGTGGTGGTGTGTGCCT   900

Query  901   GTAATCCAAGCTACTCGGGAGGCTGAGGCAGGA   933
             |||||||||||||||||||||||||||||||||
Sbjct  901   GTAATCCAAGCTACTCGGGAGGCTGAGGCAGGA   933
```

# Sequence 1382 matched with Sequence 471

Query=   Sequence ID 1382
Length=896


   SEQ ID NO: 471

ALIGNMENTS
 Identities = 896/896 (100%), Gaps = 0/896 (0%)

```
Query  1    CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTACTACCTCCAACATGAAACAAGCAGCCCCGCACTTCTCGAAGGTCTGAGTTACTTGG  60

Query  61   AATCGTTTTACCACATGATGGACAGAAGGAATATTTCAGATATCTCTGAAAACCTCAAGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AATCGTTTTACCACATGATGGACAGAAGGAATATTTCAGATATCTCTGAAAACCTCAAGC  120

Query  121  GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTACCTTCTTCAGTATTTTAAGCCAGTGATTGACAGGCAAAGCTGGAGTGACAAGGGCT  180

Query  181  CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAGTCTGGGACAGGATGCTCCGCTCGGCTCTCTTGAAGCTGGCCTGTGACCTGAACCATG  240

Query  241  CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCCAGTGGATGGAATCCAGTGGAAAAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTCCTTGCATCCAGAAAGCTGCTGAACTCTTCTCCCAGTGGATGGAATCCAGTGGAAAAT  300

Query  301  TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAAATATACCAACAGATGTTTTAAAGATTGTGTATTCTGTGGGTGCTCAGACAACAGCAG  360

Query  361  GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GATGGAATTACCTTTTAGAGCAATATGAACTGTCAATGTCAAGTGCTGAACAAAACAAAA  420

Query  421  TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTCTGTATGCTTTGTCAACGAGCAAGCATCAGGAAAAGTTACTGAAGTTAATTGAACTAG  480
```

```
Query   481   GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   GAATGGAAGGAAAGGTTATCAAGACACAGAACTTGGCAGCTCTCCTTCATGCGATTGCCA   540

Query   541   GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAGAGAAAATTGGACCCATCTTC   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   GACGTCCAAAGGGGCAGCAACTAGCATGGGATTTTGTAAGAGAAAATTGGACCCATCTTC   600

Query   601   TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   TGAAAAAATTTGACTTGGGCTCATATGACATAAGGATGATCATCTCTGGCACAACAGCTC   660

Query   661   ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTC   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   ACTTTTCTTCCAAGGATAAGTTGCAAGAGGTGAAACTATTTTTTGAATCTCTTGAGGCTC   720

Query   721   AAGGATCACATCTGGATATTTTTCAAACTGTTCTGGAAACGATAACCAAAAATATAAAAT   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721   AAGGATCACATCTGGATATTTTTCAAACTGTTCTGGAAACGATAACCAAAAATATAAAAT   780

Query   781   GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATACTTAAATGGTCA   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781   GGCTGGAGAAGAATCTTCCGACTCTGAGGACTTGGCTAATGGTTAATACTTAAATGGTCA   840

Query   841   ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA     896
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841   ATAGAAAAAGTAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA     896
```

# Sequence 1387 matched with Sequence 472

Query= Sequence ID 1387
Length=158


   SEQ ID NO: 472

ALIGNMENTS
 Identities = 158/158 (100%), Gaps = 0/158 (0%)

```
Query  1    AAAAtttttttttttttttttttttttttttttttttttttttttttttttttttttttt  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  60

Query  61   tttttttttttttttttttttttttttttttttttttttttttttCAGTGTTAAAGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGTGTTAAAGT  120

Query  121  AGGTTTGTCGACGCGGCCACGAATTTCCCGGGGACCAA  158
            ||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGGTTTGTCGACGCGGCCACGAATTTCCCGGGGACCAA  158
```

# Sequence 1389 matched with Sequence 473

Query=  Sequence ID 1389
Length=896


   SEQ ID NO: 473

ALIGNMENTS
 Identities = 896/896 (100%), Gaps = 0/896 (0%)

```
Query   1    tttttttttttttttttgggagtcagttttcttttcttttcttttctttttttttttttttgntt   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TTTTTTTTTTTTTTTGGGAGTCAGTTTTCTTTTCTTTTCTTTCTTTTTTTTTTTTTTGNTT   60

Query   61   ttCGGAAACGGAGTCTCGCTTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TTCGGAAACGGAGTCTCGCTTTCTCGCCCACTCTGGAGTGGNGCAGTGGGGNGGTCTCAG   120

Query   121  CTCACCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CTCACCACAGCCTCCACCTCCTGGGCCCAAGCGATCCTNTCACCTCAGCCTCCTGCGTAG   180

Query   181  CTGGGACTACAGGCGTGCACCACCATTCCCAGGTAATTTTTGTATTTTTTGTANANACAG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTGGGACTACAGGCGTGCACCACCATTCCCAGGTAATTTTTGTATTTTTTGTANANACAG   240

Query   241  GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GGTTTCACTGTTGTTGCCCAGGCTGGTCTCGAACTCCTGCTTCAGTCTGCCANAATGCTG   300

Query   301  GATTCTAGGCGTGAGCCACCGNGCCTGGCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GATTCTAGGCGTGAGCCACCGNGCCTGGCCCAAAAGTTACTTTTCTTACAGAAGCAAAGC   360

Query   361  TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  TTTAATGCATTTTACTGAATGCTTATAGCTTTGTAGATACTGAAAAGAGTATGAGCGTCA   420

Query   421  CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CATACAGACACATNTAACAGCACTGCCTCCAACCAGCCCCTACCCACTGGTCAGGNGAGT   480
```

```
Query  481  AANAATCAAAATTCTTTTCTGNGAGTGGAACGGAAATTTCATCTCTCCTCCTCAGGCAAG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AANAATCAAAATTCTTTTCTGNGAGTGGAACGGAAATTTCATCTCTCCTCCTCAGGCAAG  540

Query  541  TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TAGTTAANAGGCTGGNGGGAGTCATGGCCCCATTTTGTTCAAAATACAAGCTCCACAGGA  600

Query  601  ACAAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACAAAAGGCTGAACTGCTCACCTCCCAACTGATGAACCTCGTCTTTGTTCCATGTCAAAG  660

Query  661  GGGCCTTTGTGTTACTGCAGCAGAAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GGGCCTTTGTGTTACTGCAGCAGAAACTCCAGCTATCAAACCATCAGGCACCAAAAGTAA  720

Query  721  AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  AACTCCTTTCTCTAAAAAGACCTCTCTTTACCTGAGCCTTTCAATGCATCTTTGCCCCCA  780

Query  781  NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  NATAATCCTGGATGAGATAATCCCCAGAGGAANACCAGCGCTTGCCTAGTGAAATTATAC  840

Query  841  TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGGN  896
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841  TATGAGACAAGGGTAAAAGACCTCAAANACCGGGTTGGCAGGTAAGGGAGTAGGGN  896
```

Blast comparison trimmed "N" from the 3' end of both sequences and reported 895 identities. The report has been manually corrected for this. "N" has been appended to both sequences and identity count has been increased to 896.

# Sequence 1390 matched with Sequence 474

Query=   Sequence ID 1390
Length=350


    SEQ ID NO: 474

ALIGNMENTS
 Identities = 350/350 (100%), Gaps = 0/350 (0%)

```
Query  1    TCNGTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCNGTGGCACCCGTTTCCGGCACCTTCAGACTCTGAAGAGCCACCTGCGAATCCACACAGGAG  63

Query  64   AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCgggatgtgga  123
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   AGAAACCTTACCATGTACGTAAGCCTCTTGAGGCCGCTCTCTGACCTGCGGGGATGTGGA  123

Query  124  gggcagggaaggaggtggagcgcagggaaggaggtggagcagggaggcagtggaACTGTT  183
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124  GGGCAGGGAAGGAGGTGGAGCGCAGGGAAGGAGGTGGAGCAGGGAGGCAGTGGAACTGTT  183

Query  184  TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT  243
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184  TGCTCCCATCTCAAGCACACAGTGGGGCAACCACTACGCTAATGGTTGGAAGACCTAGAT  243

Query  244  CTGGGCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT  303
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  CTGGGCCCAATGGCCAGACACCCTGCTTGACCTTGGCCCAAGCATTAGGGGACTCATCTT  303

Query  304  TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT   350
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  TAAAATGAGGGTATGGGACTAGATGATCTGGGCCTTAGGAGAGGAGT   350
```


Blast comparison trimmed "TCN" from the 5' end of both sequences and reported 347
identities. The report has been manually corrected for this. "TCN" has been prepended to
both sequences and identity count has been increased to 350.

# Sequence 1391 matched with Sequence 475

Query=   Sequence ID 1391
Length=835


   SEQ ID NO: 475

ALIGNMENTS
 Identities = 835/835 (100%), Gaps = 0/835 (0%)

```
Query   1    CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAAACTCA   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    CGGCTNCTACCCTGCGGAGATCACACTGACCTGGCAGTGGGATGGGGAGGACCAAACTCA   60

Query   61   GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GGACACCGAGCTTGTGGAGACCAGGCCAGCAGGAGATGGAACCTTCCAGAAGTGGGCAGC   120

Query   121  TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTCAGCACGAGGGGCT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACGTGCCATGTTCAGCACGAGGGGCT   180

Query   181  GCCGGAGCCCCTCACCCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GCCGGAGCCCCTCACCCTGAGATGGAAGCCGTCTTCCCAGCCCACCATCCCCATCGTGGG   240

Query   241  CATCGTTGCTGGCCTGGCTGTCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  CATCGTTGCTGGCCTGGCTGTCCTGGCTGTCCTAGCTGTCCTAGGAGCTATGGTGGCTGT   300

Query   301  TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTGCTCTCAGGCTGCGTC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TGTGATGTGTAGGAGGAAGAGCTCAGGTGGAAAAGGAGGGAGCTGCTCTCAGGCTGCGTC   360

Query   361  CAGCAACAGTGCCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAAGCCTGAGACAGCTG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CAGCAACAGTGCCCAGGGCTCTGATGAGTCTCTCATCGCTTGTAAAGCCTGAGACAGCTG   420

Query   421  CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CCTGTGTGGGACTGAGATGCAGGATTTCTTCACACCTCTCCTTTGTGACTTCAAGAGCCT   480
```

```
Query  481   CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CTGGCATCTCTTTCTGCAAAGGCATCTGAATGTGTCTGCGTTCCTGTTAGCATAATGTGA   540

Query  541   GGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTG   600

Query  601   TGTTCCCTCCCCGATCATCTTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTG   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TGTTCCCTCCCCGATCATCTTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTG   660

Query  661   TCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TCTCAACTTCATGGTGCGCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCT   720

Query  721   GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   GAATATAAATTTGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAG   780

Query  781   TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG     835
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   TCAATTCCTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCANAATCCG     835
```

# Sequence 1392 matched with Sequence 476

Query=   Sequence ID 1392
Length=437


   SEQ ID NO: 476

ALIGNMENTS
 Identities = 437/437 (100%), Gaps = 0/437 (0%)

```
Query  1    TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGAAACAAAATGAATTTNTATGGGTAAGAGAGGGTAATATTTTAGAGTTGTGTTACAAAA  60

Query  61   CTACAAATTTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGttttttttCTTTCT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTACAAATTTTTATTAAATTAATAAATCAGAATACTAAATCCATGTGTTTTTTTTCTTTCT  120

Query  121  TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAAAAATATCTTTTGGCTGGGCACGGTAGCTCATGGCTGTAATCCCAGCACTTTGGGAG  180

Query  181  GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCTGAGGTGGGTGGATCGCCTGATGTCAGGAGTTCAAGACCAGCCTGGTCAACATGTTGA  240

Query  241  AACCCCATCTCTACTAAAAATATAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACCCCATCTCTACTAAAAATATAAAAATTAGCCGGTGTGGTGGTGGGCGCCTGTAATCC  300

Query  301  CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAGCTACTCAGGAGGCTAAGGCAGGAGAATTGCGTGAACCCAGGAGTTCAGTGATGTAGC  360

Query  361  GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCa  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GGGGAGCTGAGATTGTGCCACTACACTCCAGCCTGGATGACAGAGTGAGACTCCATCTCA  420

Query  421  aaaaaaaaaaaaaaaaa    437
            |||||||||||||||||
Sbjct  421  AAAAAAAAAAAAAAAAA    437
```

# Sequence 1394 matched with Sequence 477

Query=   Sequence ID 1394
Length=369


   SEQ ID NO: 477

ALIGNMENTS
 Identities = 369/369 (100%), Gaps = 0/369 (0%)

```
Query  1    GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCGTGACCCCTGTTCCC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCATAATGTGAGGAGGTGGAGAGACAGCCCACCCCCGTGTCCACCGTGACCCCTGTTCCC  60

Query  61   ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGCTGACTTGTGTTTCCTCCCCAGTCATCTTTCCTGTTCCAGAGAGGTGGGGCTGGATG  120

Query  121  TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTCCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCTTACTTCCCTACTGAA  180

Query  181  AATAAGAATCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATAAGAATCTGAATATAAATTTGTTTTCTCAAATATTTGCTATGAGAGGTTGATGGATT  240

Query  241  AATTAAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTAAATAAGTCAATTCCTGGAATTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAG  300

Query  301  aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  360

Query  361  aaaaaaaaa  369
            |||||||||
Sbjct  361  AAAAAAAAA  369
```

# Sequence 1395 matched with Sequence 478

Query=   Sequence ID 1395
Length=642


   SEQ ID NO: 478

ALIGNMENTS
 Identities = 642/642 (100%), Gaps = 0/642 (0%)

```
Query  1    CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTACCATGTCAGTGCACAGAAATGCTGTCTTGGGATGTAGGAAAAATAAATCCACAAAA  60

Query  61   GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCTACCAAGTTTGAAGGGGACCATGAGTCTTCAGGCTGGAGCTTCCAAACCAGATGAAAA  120

Query  121  CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCCCACAATTAACCTGCAGTTTAAGATCCAGCAGCTGGCCATTTCTGGACTCAAGGTGAA  180

Query  181  TCGTCTGGATATGTATGGAGAAAAGTACAAACCCTTTAAGGGCATAAAATACATGACCAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCGTCTGGATATGTATGGAGAAAAGTACAAACCCTTTAAGGGCATAAAATACATGACCAA  240

Query  241  AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTTGCTGAGGGAATAGTCTTGCAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGCTGGGAAGTTCCAAGTTCGAACCTGAAGGGAGCATTTGCTGAGGGAATAGTCTTGCAC  300

Query  301  ATTTTTTCATTTCTTACTTGTCTAAAAGTaaaaaaaaaTATCAGCCTGTCTCCTAGGTCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTTTTTCATTTCTTACTTGTCTAAAAGTAAAAAAAAATATCAGCCTGTCTCCTAGGTCA  360

Query  361  GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAACTAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTCCCCTCCTGGACCCACCCGCTCCCTTTTTTCCTTAGCCTTCAGTGCCATGGAACTAAT  420

Query  421  CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CAAGGGAGGAAAAGGTCACCAGGGAGAACTGGACAGAACTGAAACACAGCAACACCAGTT  480
```

```
Query  481  CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCAAGGACAAGGTGTGTGATGGGGGTAGGAAGCTTGGTGCTTATGTAACCATTTTAAAC  540

Query  541  GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTGGTTTCTATAGGAAAGACCAACATTTGTTTAGCTTGCTTGGCTTTAATTATCTAAAGC  600

Query  601  CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT  642
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  CAATGAAAGACTTCTTTGTTGATTTTTTAAGATAGAAAGATT  642
```

# Sequence 1396 matched with Sequence 479

Query=  Sequence ID 1396
Length=912


   SEQ ID NO: 479

ALIGNMENTS
 Identities = 912/912 (100%), Gaps = 0/912 (0%)

```
Query  1    CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAAACACTATGTTATTTTATGAANAAGACTTGAACATCTATGGATTTTGGTATTTGCAAG  60

Query  61   GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGGTGAATGGGGTATTTGCAAGCAGTGAATGAGGAGGCCTGGAACCAATCTTCTGCTGAT  120

Query  121  ATTGAGGCACAACTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAAACTGTAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTGAGGCACAACTGAAAAAGGTATATTACTTAAATCTCTTATTGTATTGTAAACTGTAT  180

Query  181  AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAAACAAT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAGTAATGAAATTAAAAGGCAGAAATTGTCAGACTGAATAAAATGAAAAGACCAAACAAT  240

Query  241  ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ATGCTGCTTACAAGAAACACAATTCAAATATAAGGACACAATTAGTTTAAAGGAAAAGAA  300

Query  301  CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTGGAAAAGATATACCATGATAACACAAGTCAGAAGAAAGCTGCTGTGGATATATTAATA  360

Query  361  TGAGATGTAGATTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGAGATGTAGATTTCAGAGCAGTGAATATTGCCAGGCATAAAGAAAGTTATTACATAATA  420

Query  421  ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACTAATATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ATTAAGGTATCAGTTCATCAAGAAGATGTAATAACCCTAAGTATTTATACAACTAATATC  480
```

Page 814

```
Query   481   AGAGCTTCAAAATACATGAAGCAAAAACCAGTGGAATTGATAGGAGAAACACACAATTAC   540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481   AGAGCTTCAAAATACATGAAGCAAAAACCAGTGGAATTGATAGGAGAAACACACAATTAC   540

Query   541   ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA   600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541   ACAATTATAGTCAGAATTTTCAACATATCTTTCTCAATGGAGAAAACAACTAGACAGGAA   600

Query   601   ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT   660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601   ATCATTAAGGATATAGATGATTTAAATTATATGATCAACTACCTGGACGTAATTGGCATT   660

Query   661   TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG   720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   661   TATGGAACACTGCACCACCAACAGCAGAGTACATATTATTTTCAAGTACACAGAAAACAG   720

Query   721   TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAAACAATTA   780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   721   TTACCAATATAGACCATTTTCTGGGTCATAAAACACATCTCAATAAATGTAAAACAATTA   780

Query   781   ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT   840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   781   ATGTTATATAAAGTATGTGCTCTGACCNCAAAGGAATTAGAGATCAATAAAAGAACATCT   840

Query   841   TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG   900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   841   TTGAAAAATCTCACNTATTTAAAAACTAATAACTCACTTCTAAATAACTCCTGTNTCAAG   900

Query   901   AGAATNAAANGG   912
              ||||||||||||
Sbjct   901   AGAATNAAANGG   912
```

Blast comparison trimmed "NGG" from the 3' end of both sequences and reported 909
identities. The report has been manually corrected for this. "NGG" has been appended to
both sequences and identity count has been increased to 912.

# Sequence 1397 matched with Sequence 480

Query=  Sequence ID 1397
Length=873


   SEQ ID NO: 480

ALIGNMENTS
 Identities = 873/873 (100%), Gaps = 0/873 (0%)

```
Query  1    CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCCAGCCTCACTGCGCCCCGTCAGGCCAGGCAGCTGCCCTCAGGGTCTGCCAAGGTGGGG  60

Query  61   GTCAAGGGCCATGGGGGCAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTCAAGGGCCATGGGGGCAGGTAGCTCTGCCTGCAAAGCCCACAAGCATGTCAGATCACC  120

Query  121  TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCCTGGCCTCGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGGCTGCAGACAGACAAACACCTGAGCTGTTCTGAATACCTTCAGGTTCCTGGCCTCGC  180

Query  181  TGAGCAAGTGCAGAAATTTTTACCTTCAAGGATCAGGgtttttctgtttgtttgtttttt  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGCAAGTGCAGAAATTTTTACCTTCAAGGATCAGGGTTTTTCTGTTTGTTTGTTTTTT  240

Query  241  AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACACACACATATGTGAACAAAGAGTATGCGTTTGTACTGGCAGAAGAAGCGTCTGGTAA  300

Query  301  GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAAttt  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GACAACCAGCAAGTTAACAATGGTCACCTCCAGAAATGGGCTGGGTAAACCAAAGAATTT  360

Query  361  ttttgtttttgttttttttGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TTTTGTTTTTGTTTTTTTTGAGTCAGGGTCTAGCTCTGTCACCCAGGCTGGAACGCACTG  420

Query  421  GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTGTGATCACGGCTCACTGCAGCCTTGACCTCCCTGGCTCAAGCAATCCTCCCAGCTCAG  480
```

```
Query  481   CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCTCCTGAGTCGTTGGGACTACAGGCACGTGCCACCACGCCTGACACATTTTTTAAATTT   540

Query  541   TTGTAGAGACAGTGTTTCACCATGTTGCCCAGGCAGGTCTCAAACTCCTGGGCTCAAGTG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TTGTAGAGACAGTGTTTCACCATGTTGCCCAGGCAGGTCTCAAACTCCTGGGCTCAAGTG   600

Query  601   GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GTCCTCCAGCTTCAGCCTCCCAAAGTGCTAGGATTATAGGTGTGAGCCACAGTGCCCAGC   660

Query  661   CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CCCGTAGTGGAGAATTTCTGTTGAATGAACCAAAAGCAACTGCCAACCTCTCCATGCACC   720

Query  721   ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   ATGTGTTTCAGAGGAGAAAGCACAGTGAAGAATGCAGTGTGTTCTGAGGTCCTGTCACCC   780

Query  781   CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CTGAGGCTGTGTGTGTCCTTTGCCAAATTAAAGAGTCTTACTGAATGCGGTGCATCCAGG   840

Query  841   AGACAGGCCNAGGTTTGGACTGGTaaaaaaaaa   873
             |||||||||||||||||||||||||||||||||
Sbjct  841   AGACAGGCCNAGGTTTGGACTGGTAAAAAAAAA   873
```

# Sequence 1399 matched with Sequence 481

Query=   Sequence ID 1399
Length=778


   SEQ ID NO: 481

ALIGNMENTS
 Identities = 778/778 (100%), Gaps = 0/778 (0%)

```
Query  1    CAGACACCTGGNAGAACGGGAAGGAGACGCTGCAGCGCGCGGACCCCCCAAAGACACATG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CAGACACCTGGNAGAACGGGAAGGAGACGCTGCAGCGCGCGGACCCCCCAAAGACACATG  60

Query  61   TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGACCCACCACCCCATCTNTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCT  120

Query  121  ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAACTCAGGACACCG  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGCGAGGACCAAACTCAGGACACCG  180

Query  181  AGCTTGTGGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGCTTGTGGGAGACCAGACCAGCAGGAGACAGAACCTTCCAGAAGTGGGCAGCTGTGGTGG  240

Query  241  TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGC  300

Query  301  CCCTCACCCTGAGATGGGAGCCATCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTTG  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCCTCACCCTGAGATGGGAGCCATCTTCCCAGTCCACCGTCCCCATCGTGGGCATTGTTG  360

Query  361  CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTGGTCGCTGCTGTGATGTGTA  420

Query  421  GGAGGAAGAGTTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGAGGAAGAGTTCAGGTGGAAAAGGAGGGAGCTACTCTCAGGCTGCGTCCAGCGACAGTG  480
```

```
Query  481  CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CCCAGGGCTCTGATGTGTCTCTCACAGCTTGAAAAGCCTGAGACAGCTGTNTTGTGAGGG  540

Query  541  ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACTGAGATGCAGGATTTCTTCACGCCTCCCCTTTGTGACTTCAAGAGCCTCTGGCATCTC  600

Query  601  TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTTCTGCAAAGGCACCTGAATGTGTCTGCGTCCTTGTTAGCATAATGTGAGGAGGTGGAG  660

Query  661  AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  AGACAGCCCACCCTTGTGTCAACTGTGACCCCCTGTTCCCATGCTGACCTGTGTTTCCTC  720

Query  721  CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA  778
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  CCCAGTCATCTTTTTTGTTCNCAATAGGTGGGGCCTGGATGTCTCCATCTCTGTNTCA  778
```

# Sequence 1440 matched with Sequence 482

Query=   Sequence ID 1440
Length=666


   SEQ ID NO: 482

ALIGNMENTS
 Identities = 666/666 (100%), Gaps = 0/666 (0%)

```
Query  1    TTATAAGGTACTTTTAAGGTATTTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTATAAGGTACTTTTAAGGTATTTTAGTTGTCTTAGTCTATATTTCTGTACTCACCTTTC  60

Query  61   TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCCATATCTTTGCAATTCTGAAT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTTATCCACTCATCAGTTGATGGGCATGTAGGTTGGTTCCATATCTTTGCAATTCTGAAT  120

Query  121  TGTGCTGTGATCAGGTGTCTTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGTGCTGTGATCAGGTGTCTTTTTAGTATAATGATTTACTCTCCTTTGGGTAGATACCCA  180

Query  181  GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTAGTGGGATTGCTGGATCGAATGGTTTTTATAATTTTCTATTTTACCACAGTTTCTCTC  240

Query  241  TGCATTTTTCCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGCATTTTTCCTCTTTGACCACTAACCATGTGAAATTCTCATATTGACCTTTATAATGAT  300

Query  301  CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATGAACTCTTAGTATCATTGGGAAGGCCACATTTGCCACTTATGATTGTAAACCTTATC  360

Query  361  CTCCATTTTTCCTGTTATTGTTGGTGCAAAAAGCACCTATTATACCAGGACTTTAAAAAT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCCATTTTTCCTGTTATTGTTGGTGCAAAAAGCACCTATTATACCAGGACTTTAAAAAT  420

Query  421  CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CAGTCTGATAAGTCTTTGATAAGTCTAATAATAATAACTGATAAGTCCATTGAATTTGCT  480
```

```
Query  481  TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCTGATTACTTTTTCTTTAGTAGCTAAACATGTATGTACTCCTATGATTACAATGAACAC  540

Query  541  TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCCTCTCCATTTAAATTAATTATTTACATTGATGAAATAGCAAAATGTTAATGACTAAAT  600

Query  601  ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACTTCTTATAATTTTCttttttt  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  ACTGTCTTGGTTTTTTCGTTCCAGGTCAGTCAATATTAACTTCTTATAATTTTCTTTTTT  660

Query  661  ttCTTT  666
            ||||||
Sbjct  661  TTCTTT  666
```

## Sequence 1447 matched with Sequence 483

Query= Sequence ID 1447
Length=630


   SEQ ID NO: 483

ALIGNMENTS
 Identities = 630/630 (100%), Gaps = 0/630 (0%)

```
Query  1    GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGA  60

Query  61   GAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACA  120

Query  121  CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAGC  180

Query  181  CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCACAGAA  240

Query  241  CCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTCTTTGGACAC  300

Query  301  TAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTAGGCCTAAAAGCAG  360

Query  361  CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAAAAAATCCCAAACATATA  420

Query  421  ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACTGAACTCCTCACACCCAATTGGACCAATCTATCACCCTATAGAAGAACTAATGTTAGT  480
```

```
Query  481  ATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATAAGTAACATGAAAACATTCTCCTCCGCATAAGCCTGCGTCAGATTAAAACACTGAACT  540

Query  541  GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GACAATTAACAGCCCAATATCTACAATCAACCAACAAGTCATTATTACCCTCACTGTCAA  600

Query  601  CCCAACACAGGCATGCTCATAAGGAAAGGT  630
            ||||||||||||||||||||||||||||||
Sbjct  601  CCCAACACAGGCATGCTCATAAGGAAAGGT  630
```

# Sequence 1448 matched with Sequence 484

Query=   Sequence ID 1448
Length=612


   SEQ ID NO: 484

ALIGNMENTS
 Identities = 612/612 (100%), Gaps = 0/612 (0%)

```
Query  1    GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGCCACCGGGTGCAAGGTCAGGGCTGGGGTGGAGGCTGGGAAGCCCAGGGCTTGGCCCAC  60

Query  61   TGTGGCCGCCTTGTGTGGTCACTGCTTTCCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTGGCCGCCTTGTGTGGTCACTGCTTTCCTGGGCCTGCTGTGAGCTCCCTCTAGGACCC  120

Query  121  CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CAGGCCTGTCTGGTGGGTCACTGTGACCACCACCTTGCACAGCACCTGGCGCGTGGCAGG  180

Query  181  TGCTCAAACATTACTTGTTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTTGACTAATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCTCAAACATTACTTGTTTCGGAATGAACTTCATCTTGCTCTTGGCTTTTTGACTAATG  240

Query  241  CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCCAGTTTCCCAGCTATAAAGT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTGTGGAACATCTGACTAATTAGTGACTCTTTGGGGCCCCCAGTTTCCCAGCTATAAAGT  300

Query  301  GGTAATATTAAGATAATAATTCGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GGTAATATTAAGATAATAATTCGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCAGC  360

Query  361  ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ACTTTGGGAGGCCGAGGTGGGCAGATCACGAGGTCAGAAGATCGAGACCATCCTGGCTAA  420

Query  421  CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CACGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTANCCGGGCGTGGTGGCGGGCG  480
```

```
Query  481   CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCTGTAGTCCCAGCTACTCANGAGGCTGANGCAGGAGAATGGTGTGAACCCGGGAGGCAG   540

Query  541   AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGGTTGCAGTGAACCAAGATCGNNCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTC   600

Query  601   CATCTTAAAAAA   612
             ||||||||||||
Sbjct  601   CATCTTAAAAAA   612
```

# Sequence 1449 matched with Sequence 485

```
Query=   Sequence ID 1449
Length=362


   SEQ ID NO: 485

ALIGNMENTS
 Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query  1    AATCAGGGCCGCAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATTTAACCGCTGGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AATCAGGGCCGCAGTGTGTTCTGCGCCTGCCCAGAGCTGACTCCTGATTTAACCGCTGGC  60

Query  61   GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTCACCCTCACGTGGTTTCTTTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GTAACCGCGGGTTGCACGCATGCGTGCTGAAAAGCCTTTCACCCTCACGTGGTTTCTTTT  120

Query  121  TTAACCAGTCATCAAGCGAGGCTCGCGCGCAGGCCCCGCGTTGGAAAATGGCGGGGAAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTAACCAGTCATCAAGCGAGGCTCGCGCGCAGGCCCCGCGTTGGAAAATGGCGGGGAAGC  180

Query  181  TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAAACCTCTGAATGTGGAGGCGCCAGAAGCTGCTGAGGAGGCTGAAGGTAGTGAGGGCA  240

Query  241  AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGTGGGCTGCACTCCTTTCTCTCCAACCAGGGCAGAAAGGAGGGAGGATTCGTCCCATTA  300

Query  301  CAATAATGAAATAATGATATTCTAAtttttttAAATAAAATGTTAAGCCTTTTGTTATTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAATAATGAAATAATGATATTCTAATTTTTTTAAATAAAATGTTAAGCCTTTTGTTATTG  360

Query  361  AA  362
            ||
Sbjct  361  AA  362
```

# Sequence 1450 matched with Sequence 486

Query=   Sequence ID 1450
Length=854


   SEQ ID NO: 486

ALIGNMENTS
 Identities = 854/854 (100%), Gaps = 0/854 (0%)

```
Query  1    GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GGAAANCATGAGGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTC   60

Query  61   CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGGCGTCACCCT   120

Query  121  CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCCTGCCCCAACTGGTCGGAGTCTCCAC   180

Query  181  ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACCGCTGCAGGGCGGCTCGAACAGTGCCGCCGCCATCGGGCAGTCCTCCGGGGAGCTCCG   240

Query  241  GACCGGAGGGGCCCGGCCGCCGCCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG   300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACCGGAGGGGCCCGGCCGCCGCCTCCTNTAGGCGCCTCCTCCCAGCCGCGCCCGGGTGG   300

Query  301  CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CGACTCCAGCCCAGTCGTGGATTCTGGCCCTGGCCCCGCTAGCAACTTGACCTCGGTCCC   360

Query  361  AGTGCCCCACACCACCGCACTGTCGCTGCCCGCCTGCCCTGAGGAGTCCCCGCTGCTTGG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGTGCCCCACACCACCGCACTGTCGCTGCCCGCCTGCCCTGAGGAGTCCCCGCTGCTTGG   420

Query  421  TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGAcccccccGGATTTCCCCGACAGGG   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAGGACTCGGGTCGGCGCCAGTCGGAGGATTGGGACCCCCCCGGATTTCCCCGACAGGG   480
```

```
Query  481   TCCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TCCCCCANACATTCCCTCAGGCTGGCTCTTCTACGACAGCCAGCCTCCCTCTTCTGGATC   540

Query  541   AGAGTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCGAGGTGG   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGAGTTTTAAATCCCANACAGAGGCTTGGGACTGGATGGGAGAGAAGGTTTGCGAGGTGG   600

Query  601   GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GTCCCTGGGGAGTCCTGTTGGAGGCGTGGGGCCGGGACCGCACAGGGAAGTCCCGAGGCC   660

Query  661   CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CCTCTAGCCCCAAAACCANAGAAGGCCTTGGAGACTTCCCTGCTGTGGCCCGAGGCTNAG   720

Query  721   GAAGTTTTGGAGTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   GAAGTTTTGGAGTTTTGGGTCTGCTTANGGCTTCNAGCAGCCTTGCACTGAGAACTTTGG   780

Query  781   TAGGGACCTCGAGTAATCCACTCCNTTTTNGGGACTGACGTGAGGCTCCCGGTGGGGAAA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   TAGGGACCTCGAGTAATCCACTCCNTTTTNGGGACTGACGTGAGGCTCCCGGTGGGGAAA   840

Query  841   GANACTGACCTNTC   854
             ||||||||||||||
Sbjct  841   GANACTGACCTNTC   854
```

Blast comparison trimmed "NTC" from the 3' end of both sequences and reported 851 identities. The report has been manually corrected for this. "NTC" has been appended to both sequences and identity count has been increased to 854.

# Sequence 1453 matched with Sequence 487

Query=  Sequence ID 1453
Length=843


   SEQ ID NO: 487

ALIGNMENTS
 Identities = 843/843 (100%), Gaps = 0/843 (0%)

```
Query  1    CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGACCTGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCTGG  60

Query  61   AGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGAATGGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGAATGGAA  120

Query  121  AGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAAGTTGACT  180

Query  181  TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTCAGCAAGG  240

Query  241  ACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGATGAGTATG  300

Query  301  CCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGATCGAGACA  360

Query  361  TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTCCAAATTC  420

Query  421  TGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACAAAATGTA  480
```

```
Query  481  GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAGTGCTGTC  540

Query  541  TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACT  600

Query  601  TAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGATTTGAACT  660

Query  661  CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CTTCAATCTCTTGCACTCAAAGCTTGTTAAGATAGTTAAGCGTGCATAAGTTAACTTCCA  720

Query  721  ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  ATTTACATACTCTGCTTAGAATTTGGGGGAAAATTTAGAAATATAATTGACAGGATTATT  780

Query  781  GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  GGAAATTTGTTATAATGAATGAAACATTTTTGTCATATAAGATTCATATTTACTTCTTAT  840

Query  841  ACA  843
            |||
Sbjct  841  ACA  843
```

# Sequence 1454 matched with Sequence 488

Query=   Sequence ID 1454
Length=578


   SEQ ID NO: 488

ALIGNMENTS
 Identities = 578/578 (100%), Gaps = 0/578 (0%)

```
Query  1    TAAATAGGGAATCCTTTCCCCATTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TAAATAGGGAATCCTTTCCCCATTGCTTGTTTTTCTCAGGTTTGTCAAAGATCAGATAGT  60

Query  61   TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGTAGATATGCGACGTTATTTCTGAGGGCTCTGTTCTGTTCCATTGATCTATATCTCTGT  120

Query  121  CACATGCACACGTATGTTTGTTGTGGCACTATTCACAGTGGCAAAGACTTGGAACCAACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CACATGCACACGTATGTTTGTTGTGGCACTATTCACAGTGGCAAAGACTTGGAACCAACC  180

Query  181  CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CAAATGTCCAACAATGATAGACCGGGTTAAGAAAATGCGGCACATATACACCATGGAATA  240

Query  241  CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTATGTAGCCATAAAAAATGATGAGTTCGTGTCCTTTGTAGGGACATGGATGAAATTGGA  300

Query  301  AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAAACCAAACACTGCATATTCTCACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AATCATCATTCTCAGTAAACTATCGCAGGAACAAAAAACCAAACACTGCATATTCTCACT  360

Query  361  CATAGGTGGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CATAGGTGGGAATTGAACAGTGGGAACACATGGACACAGGAAGGGGAACATCACACTCTG  420

Query  421  AGGACTGTTGTGGGGTGGGGGGAGGGAGGAGGGGGATAGCATTGGGAGATATACCTAGTGCT  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGGACTGTTGTGGGGTGGGGGGAGGGAGGAGGGGGATAGCATTGGGAGATATACCTAGTGCT  480
```

```
Query  481   GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAACTAAC   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GGATGACGAGTTAGTGGGTGCAGCGCACCAGCATGTCACATGTATACATATGTAACTAAC   540

Query  541   CTGCACATTGTGCACATGTACCCTAAAACTTAAGGTAT   578
             ||||||||||||||||||||||||||||||||||||||
Sbjct  541   CTGCACATTGTGCACATGTACCCTAAAACTTAAGGTAT   578
```

# Sequence 1456 matched with Sequence 489

Query=   Sequence ID 1456
Length=628


   SEQ ID NO: 489

ALIGNMENTS
 Identities = 628/628 (100%), Gaps = 0/628 (0%)

```
Query  1    CCGCAACAAACACGGGAGTGCAGATATCGCTGCGATGGGCTGATTTCCTTTATTTGGGTA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGCAACAAACACGGGAGTGCAGATATCGCTGCGATGGGCTGATTTCCTTTATTTGGGTA   60

Query  61   TATACCCAGCAGTGGGATTGCTGGATTGTATGGTAGCTCTATTAGTTTTTTGAGGAACCT   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TATACCCAGCAGTGGGATTGCTGGATTGTATGGTAGCTCTATTAGTTTTTTGAGGAACCT   120

Query  121  CCAAACTGTTCTNCATAGTGGTTGTACTCATTTACATTCCCACTGTGAACCCTGAAAATT   180
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAAACTGTTCTNCATAGTGGTTGTACTCATTTACATTCCCACTGTGAACCCTGAAAATT   180

Query  181  TGAGGCAGGTCTCAGTTAAATTAGAAAGTTGATTTTGCCAAGTTGGGGACACGCACTCGT   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGAGGCAGGTCTCAGTTAAATTAGAAAGTTGATTTTGCCAAGTTGGGGACACGCACTCGT   240

Query  241  GACACAGCCTCAGGAGGAACTGATGACATGTGCCCAGGTGGTCAGAGCACAGCTTGGTTT   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GACACAGCCTCAGGAGGAACTGATGACATGTGCCCAGGTGGTCAGAGCACAGCTTGGTTT   300

Query  301  TATACATTTTAGGGAAACCTGAGCCATCAATCAACATACGTAAAATGGGCCGGGCACAGC   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TATACATTTTAGGGAAACCTGAGCCATCAATCAACATACGTAAAATGGGCCGGGCACAGC   360

Query  361  AGCTCAAGCTGTAATCCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACTTGAGGTCAG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGCTCAAGCTGTAATCCCAGCACTCTGGGAGGCCGAGGCGGGTGGATCACTTGAGGTCAG   420

Query  421  GAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTATTAAAAATACAAAGCT   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTATTAAAAATACAAAGCT   480
```

```
Query  481   TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TAGCTGGATGTGGTGGCGCATGCCTGTAGTCCCAGCTGCTCTAGGAGGCTGAGGCATGAG   540

Query  541   AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AATTGCTTGAACCTGGGAGGCAGAGGCTGCAGTGAGCCGAGATCGAGCCACTATACTCCA   600

Query  601   GCCTGGTCAACAGAGTGAGACCCTGTCT   628
             ||||||||||||||||||||||||||||
Sbjct  601   GCCTGGTCAACAGAGTGAGACCCTGTCT   628
```

# Sequence 1460 matched with Sequence 490

Query= Sequence ID 1460
Length=612


   SEQ ID NO: 490

ALIGNMENTS
 Identities = 612/612 (100%), Gaps = 0/612 (0%)

```
Query  1    CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCACAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGA  60

Query  61   GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGC  120

Query  121  CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTTGGGGA  180

Query  181  TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAAGT  240

Query  241  GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGGCACCTTTGCCAC  300

Query  301  ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGCTCCTGGG  360

Query  361  CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCA  420

Query  421  GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTA  480
```

```
Query  481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTA  540

Query  541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACAT  600

Query  601  TTATTTTCATTG  612
            ||||||||||||
Sbjct  601  TTATTTTCATTG  612
```

# Sequence 1490 matched with Sequence 491

Query=   Sequence ID 1490
Length=677


    SEQ ID NO: 491

ALIGNMENTS
 Identities = 677/677 (100%), Gaps = 0/677 (0%)

```
Query   1    ATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAAACCGGGGGCAAGAGAAAGCCC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    ATGGGCATCTCTCGGGACAACTGGCACAAGCGCCGCAAAACCGGGGGCAAGAGAAAGCCC   60

Query   61   TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TACCACAAGAAGCGGAAGTATGAGTTGGGGCGCCCAGCTGCCAACACCAAGATTGGCCCC   120

Query   121  CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CGCCGCATCCACACAGTCCGTGTGCGGGGAGGTAACAAGAAATACCGTGCCCTGAGGTTG   180

Query   181  GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAAACAAGGATCATCGAT   240
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct   181  GACGTGGGGAATTTCTCCTGGGGCTCANAGTGTTGTACTCGTAAAACAAGGATCATCGAT   240

Query   241  GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACCAAGACCCTGGTGAAGAATTGC   300

Query   301  ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATCGTGCTCATCGACAGCACACCGTACCGACAGTGGTACGAGTCCCACTATGCGCTGCCC   360

Query   361  CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTaaacaaaaaa   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTGGGCCGCAAGAAGGGAGCCAAGCTGACTCCTGAGGAAGAAGAGATTTTTAAACAAAAA   420

Query   421  cgatctaaaaaaattcagaagaaatatgatgaaaggaaaaagaatgccaaaatCAGCAGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CGATCTAAAAAAATTCAGAAGAAATATGATGAAAGGAAAAAGAATGCCAAAATCAGCAGT   480
```

```
Query  481  CTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCCTGGAGGAGCAGTTCCAGCAGGGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGA  540

Query  541  CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAGTGTGGCCGAGCAGATGGCTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGG  600

Query  601  AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAAATCAAGGCCCGCAAAGGCAAATAAATCCTTGTTTTGTCTTCACCCATGTAATAAAGG  660

Query  661  TGTTTATTGTTTTTGTT    677
            |||||||||||||||||
Sbjct  661  TGTTTATTGTTTTTGTT    677
```

# Sequence 1491 matched with Sequence 492

Query=   Sequence ID 1491
Length=736


   SEQ ID NO: 492

ALIGNMENTS
 Identities = 736/736 (100%), Gaps = 0/736 (0%)

```
Query    1    CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1    CTTNCACATACTGATTGATGTCTCATGTCTCTCTAAAATGTGTAAAACCAAGCTGTGCCC   60

Query    61   CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCATGGGCACACCTTAA   120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    61   CAACCACCTTGGGNACATGTGGNGAGGACCTCCTGAGGCTGTGTCATGGGCACACCTTAA   120

Query    121  CCCTGGGAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC   180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    121  CCCTGGGAAAATAAACTTTCTAAACTGACTTGAGAGCTGTCTCAGATATTCTGAGCTTAC   180

Query    181  AGTTATTGTGAAATCATTTTAATTATAAATTAAGTGGAGATTTACTTAAAATCATGTGTA   240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    181  AGTTATTGTGAAATCATTTTAATTATAAATTAAGTGGAGATTTACTTAAAATCATGTGTA   240

Query    241  GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    241  GAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCATCTTATGTATCTTCCCTCCC   300

Query    301  TCTTCCAGGTTCTGATAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    301  TCTTCCAGGTTCTGATAAAAACAGATGAAATCTGAAAGACCATGACAGTAGTATTTTGAA   360

Query    361  AATGACAGTATTTGAAATTAAAAAATTGTAAAAGTGTTCTGTTCTATCACTGCCAAAGGA   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    361  AATGACAGTATTTGAAATTAAAAAATTGTAAAAGTGTTCTGTTCTATCACTGCCAAAGGA   420

Query    421  TAAGTTACAAATTGGTTCTTGGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT   480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    421  TAAGTTACAAATTGGTTCTTGGAACGTAATATGTACTATGTGCTTGCTATTTAATAATTT   480
```

```
Query  481  ACCAGTCTTAGTCTTTTTTATTCAGACTAATTTTACCttttttttAACCTATGACTCtttA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACCAGTCTTAGTCTTTTTTATTCAGACTAATTTTACCTTTTTTTAACCTATGACTCTTTA  540

Query  541  gttatagtagtacaaaaaagtagttttagttatagttttagttgtagtacaaaaaaGCAT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTTATAGTAGTACAAAAAAGTAGTTTTAGTTATAGTTTTAGTTGTAGTACAAAAAAGCAT  600

Query  601  TTTCTGTAAGCTTAATTTCTTTCCCCTTCCCGCTTTCCCAGTCAGATGACTTTAGTGATT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  TTTCTGTAAGCTTAATTTCTTTCCCCTTCCCGCTTTCCCAGTCAGATGACTTTAGTGATT  660

Query  661  TGGAGTTGTGTGCTTTATAAGTGCATTCCTCAGAGGACTTAATATTACTAAGATTTTAGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  TGGAGTTGTGTGCTTTATAAGTGCATTCCTCAGAGGACTTAATATTACTAAGATTTTAGC  720

Query  721  AACNCTGAAATATGTT  736
            ||||||||||||||||
Sbjct  721  AACNCTGAAATATGTT  736
```

# Sequence 1492 matched with Sequence 493

Query=   Sequence ID 1492
Length=579


   SEQ ID NO: 493

ALIGNMENTS
 Identities = 579/579 (100%), Gaps = 0/579 (0%)

```
Query  1     TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TGTNCCTGTAGTCCTGTGTGGGAGGATTGCCTGAGCCTAGGAGCTCAAAGTTGCAGTGAG   60

Query  61    CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCaaaaaaa   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCCAGATCGNGNCATTGCAGTCCAGCCTGGGTGACAGAGTGAGACCCCATGTCAAAAAAA   120

Query  121   aaaaaacaaaaaaCAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AAAAAACAAAAAACAGGGGCCTGCCTCANCCAGCAGGTGAGGTCTGCCACTGAGAGCACT   180

Query  181   TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTCAGCCTTA   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TCTAGCAGCAGGAACAGCCTCCACCCCCACACTGCAATCAAGTTTTTTGGGTCAGCCTTA   240

Query  241   GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGAGCTAANAAAGGGCCTAGTTTGNCTAAATAGCAGGAGTTATATCCAGGGATCTTCAGG   300

Query  301   CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   CCCAGGAATGCTAATGAGTAGGCATTCCATGGGCCCTGGGAATGGCTTTGTGTGCCANAA   360

Query  361   ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATGATGGCCACAAAGGCCTTGCTGCCTTTTTTCAAAATGGCTGCATCCAGCTGAGTGCTC   420

Query  421   TCTGCCAAAGGGGanaanaaaaTAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCTGCCAAAGGGGANAANAAAATAAGTCTCCAGTGCATTTAGATTGGTCTCTCATCATCT   480
```

```
Query  481  CTCTCCTTTTTGTTTTTATTAGTCTCCTTAACCAAAACTGCCAAGAAAGGCTTGGAATTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTCTCCTTTTTGTTTTTATTAGTCTCCTTAACCAAAACTGCCAAGAAAGGCTTGGAATTG  540

Query  541  AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT  579
            |||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAACAAAACCTGATANAANAGGTAAGAGGTTGTTCTTTT  579
```

# Sequence 1493 matched with Sequence 494

Query= Sequence ID 1493
Length=752


   SEQ ID NO: 494

ALIGNMENTS
 Identities = 752/752 (100%), Gaps = 0/752 (0%)

```
Query  1    TGTNTCaaaaaaaaaaaaaaGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TGTNTCAAAAAAAAAAAAAAAGAACGGNAATGTACTGGAGATGTATTTGATAACCAAGGNT  60

Query  61   TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAACTGAAAAATGTTGTAGGCTTAA  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTAGGTAAATTTTCACCAGTATTAGTTNTATTTGCAAACTGAAAAATGTTGTAGGCTTAA  120

Query  121  TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATAAAATAACCACATTAGTGAACATTATATCTCTTAGAAGAAAGGCCATATTTTGCTCC  180

Query  181  TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TGCTTCTGTAAAAATATTATTTGTTTGAAGGGGAAATAATGGTAGTGTGACCTTTCACTT  240

Query  241  AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAATTCTGGAGT  300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AATTCCTACTCCCTTAATGTGAGAGAGACAAAATGAGCTGAAGAAGGAAAATTCTGGAGT  300

Query  301  TACACTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT  360
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACACTCCACAACCTTGAACATACTGACGGACATCTCTGTTTTGACAACGATTTCTCCAT  360

Query  361  GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA  420
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCACCCATGCTNTAATGCCTTGTGGATCACGGACAACCCTCTTTGCACAAGCTACAGCA  420

Query  421  TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAACTGCTCCT  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TCAGCGATGTTATCTTGCAGCAAAGCACTGCAGGATAAATGACAGGCATTAACTGCTCCT  480
```

```
Query  481  GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGGGTTTTGCCATCATTACACCAGTAGCGGCTATTGATCTGAAATATCCCATAATCAGTG  540

Query  541  CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTTGGCC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CTTCTGTCTCCAGCATTGTAGTTTGTAGCTCGTGTGTTGTAACCACTCTCCCATTTGGCC  600

Query  601  AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  AAACACATCCAGTTTGCTAGGCTGATTCCCCTGTAGCCATCCATTCCCAATCTTTTCAGA  660

Query  661  GTTCTGGCCAACTCACACCTTTCAAAGACCTTGCCCTGGACCGTAACAGAAAGGAGGACA  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  GTTCTGGCCAACTCACACCTTTCAAAGACCTTGCCCTGGACCGTAACAGAAAGGAGGACA  720

Query  721  AGCCCCAGAACAATGAGAGCCTTCATGTTGAC  752
            ||||||||||||||||||||||||||||||||
Sbjct  721  AGCCCCAGAACAATGAGAGCCTTCATGTTGAC  752
```

# Sequence 1494 matched with Sequence 495

Query=   Sequence ID 1494
Length=414


   SEQ ID NO: 495

ALIGNMENTS
 Identities = 414/414 (100%), Gaps = 0/414 (0%)

```
Query  1    TTGGTACCCGGGAAATTCTTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTGGTACCCGGGAAATTCTTTGCCGCGTCGACGGCCGGTGAGGCAGATCACCTGAGCCCA  60

Query  61   GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGAGTTCAGGACCAGCCTGGGCAGCATACCGGGATTCCATCTNNACTAAAAACAGTAGGC  120

Query  121  TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TGGGTGTGGTGGCTCATGTCTGTAAGCTCAGGACTTTGGAAGGCCAAGATGGGAGGATCA  180

Query  181  CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTTGAGCCTGGGAGTTTGACACCAGCTTGAGCATCGTAGCCAGGCCCTGACTCTACAAAA  240

Query  241  AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGTGAAATAATTAGCCGAGTGTGGTGGTTCACACCTGTAATCCCAGCTGCTCAGGAGGC  300

Query  301  TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAGGTAGGAGAATCATTTGAACCCGGGAGGTGGAGGTTGCAGTTAGCCGAGATCACGCC  360

Query  361  ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCaaaaaaaaaaaaaa    414
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTGCACTCCGGCCTGGGCGATAAAGCGAGACTCTGTCTCAAAAAAAAAAAAAA    414
```

# Sequence 1495 matched with Sequence 496

Query=    Sequence ID 1495
Length=670


    SEQ ID NO: 496

ALIGNMENTS
 Identities = 670/670 (100%), Gaps = 0/670 (0%)

```
Query   1    ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    ATTCGGGCCGAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCT   60

Query   61   GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAG   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GGCCTGGAGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAG   120

Query   121  AATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATTGAA   180

Query   181  GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTC   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTTGTCTTTC   240

Query   241  AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGAT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCACTGAAAAAGAT   300

Query   301  GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGAT   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAGATAGTTAAGTGGGAT   360

Query   361  CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGCATTTGGATTGGATGAATTC   420

Query   421  CAAATTCTGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACA   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAAATTCTGCTTGCTTGCTTTTTAATATTGATATGCTTATACACTTACACTTTATGCACA   480
```

```
Query  481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AAATGTAGGGTTATAATAATGTTAACATGGACATGATCTTCTTTATAATTCTACTTTGAG  540

Query  541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGCTGTCTCCATGTTTGATGTATCTGAGCAGGTTGCTCCACAGGTAGCTCTAGGAGGGCT  600

Query  601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCACCTTAGAGGTGGGGAGCAGAGAATTCTCTTATCCAACATCAACATCTTGGTCAGAT  660

Query  661  TTGAACTCTT  670
            ||||||||||
Sbjct  661  TTGAACTCTT  670
```

## Sequence G6 matched with Sequence 497

```
Query=   Sequence ID G6
Length=489


   SEQ ID NO: 497

ALIGNMENTS
 Identities = 489/489 (100%), Gaps = 0/489 (0%)

Query   1    GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTCGCTCTCGCCGAGGAAC   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTCGCTCTCGCCGAGGAAC   60

Query   61   AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   AAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCGGAAAAACACC   120

Query   121  CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCCTAACAAGCCGCAACGTAAA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCCTAACAAGCCGCAACGTAAA   180

Query   181  ATCCTTGGAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAATCTCAAAGT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  ATCCTTGGAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGAATCTCAAAGT   240

Query   241  GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAAACTCCTTG   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAAAAACTCCTTG   300

Query   301  TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  TGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGCGACTCATTGA   360

Query   361  CTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTGAGCCAGGAGT   420

Query   421  TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAATTGATGACCAG   480
```

```
Query  481  TTGTTAAAA  489
            |||||||||
Sbjct  481  TTGTTAAAA  489
```

# Sequence 61 matched with Sequence 498

```
Query=   Sequence ID - 61
Length=362


   SEQ ID NO: 498


ALIGNMENTS
 Identities = 362/362 (100%), Gaps = 0/362 (0%)

Query  1    CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTTATTGAAAATTTTACTAATTTCTTACTTTTTAGGTTTTAGGAGAATACTTTTGGATAA  60

Query  61   TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TTGACTAGCCTCACATTATATTGATAGAGGTTCTTGAAAACTTTAATGCCAATTCATGTA  120

Query  121  TCTTATGACTAAAATAGATAATCCATTTAGAAATTTAAGTCATTCTTGCGTGCTTGATAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TCTTATGACTAAAATAGATAATCCATTTAGAAATTTAAGTCATTCTTGCGTGCTTGATAT  180

Query  181  GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTGTCAGCACTATCCAAGTTGCTAGGGGATACAATGGTGAAGTGAAAATATCAGCTAGGT  240

Query  241  GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCCGGTGGCTCACACCTGTTATCCCAACAGTTTGGGAGGCCAGGGTGGGAGGATCACTCA  300

Query  301  AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AGCACANGCGTTTCACACCAGCCTGGACAACATACAAGACCCCATCTTTACCAAAAGTTA  360

Query  361  AG  362
            ||
Sbjct  361  AG  362
```

## Sequence 77 matched with Sequence 501

Query= Sequence ID - 77
Length=464

  SEQ ID NO: 501

ALIGNMENTS
 Identities = 464/468 (99%), Gaps = 4/468 (0%)

```
Query  1    GCGGCTGCTGTTGGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCGGCTGCTGTTGGTTGGGGGCCGTCCCGCTCCTAAGGCAGGAAGATGGTGGCCGCAAAG  60

Query  61   AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AAGACGAAAAAGTCGCTGGAGTCGATCAACTCTAGGCTCCAACTCGTTATGAAAAGTGGG  120

Query  121  AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAGTACGTCCTGGGGTACAAGCAGACTCTGAAGATGATCAGACAAGGCAAAGCGAAATTG  180

Query  181  GTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GTCATTCTCGCTAACAACTGCCCAGCTTTGAGGAAATCTGAAATAGAGTACTATGCTATG  240

Query  241  TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCA---  297
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATATTGAACTGGGCACAGCAGCA  300

Query  298  TGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATTGATCCAGGTGACTCTGACATC  360

Query  358  ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTA-AACCTTTTCACCTACAAAATTTCA  416
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  361  ATTAGAAGCATGCCAGAACAGACTGGTGAAAAGTANAACCTTTTCACCTACAAAATTTCA  420

Query  417  CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTG  464
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CCTGCAAACCTTAAACCTGCAAAATTTTCCTTTAATAAAATTTGCTTG  468
```

## Sequence 490 matched with Sequence 499

Query= Sequence ID - 490
Length=382

  SEQ ID NO: 499

ALIGNMENTS
 Identities = 382/382 (100%), Gaps = 0/382 (0%)

```
Query  1    TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCCAGCA  60

Query  61   CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAGCCTGGCCA  120

Query  121  ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGCGCATG  180

Query  181  CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTTTGAACCCGGGAGGCGG  240

Query  241  AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAAACTC  300

Query  301  CATCTCaaaaaaaaaaaaaaaaaaaCAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATCTCAAAAAAAAAAAAAAAAAAAAACAACCTTTATTTTTTCTGATTTTAAAAGTAATAACT  360

Query  361  AGTTTGTAGAAACATTAAAAGT  382
            ||||||||||||||||||||||
Sbjct  361  AGTTTGTAGAAACATTAAAAGT  382
```

# Sequence 892 matched with Sequence 500

Query=  Sequence ID – 892
Length=556


   SEQ ID NO: 500

ALIGNMENTS
 Identities = 556/556 (100%), Gaps = 0/556 (0%)

```
Query  1    TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGCGGTCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTCGACGCGGTCG  60

Query  61   TAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTCGCTCTC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TAAGGGCTGAGGATTTTTGGTCCGCACGCTCCTGCTCCTGACTCACCGCTGTTCGCTCTC  120

Query  121  GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GCCGAGGAACAAGTCGGTCAGGAAGCCCGCGCGCAACAGCCATGGCTTTTAAGGATACCG  180

Query  181  GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCCTAACAAGCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAAAAACACCCGTGGAGCCGGAGGTGGCAATTCACCGAATTCGAATCACCCTAACAAGCC  240

Query  241  GCAACGTAAAATCCTTGGAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCAACGTAAAATCCTTGGAAAAGGTGTGTGCTGACTTGATAAGAGGCGCAAAAGAAAAGA  300

Query  301  ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATCTCAAAGTGAAAGGACCAGTTCGAATGCCTACCAAGACTTTGAGAATCACTACAAGAA  360

Query  361  AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAACTCCTTGTGGTGAAGGTTCTAAGACGTGGGATCGTTTCCAGATGAGAATTCACAAGC  420

Query  421  GACTCATTGACTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GACTCATTGACTTGCACAGTCCTTCTGAGATTGTTAAGCAGATTACTTCCATCAGTATTG  480
```

```
Query  481  AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AGCCAGGAGTTGAGGTGGAAGTCACCATTGCAGATGCTTAAGTCAACTATTTTAATAAAT  540

Query  541  TGATGACCAGTTGTTT  556
            ||||||||||||||||
Sbjct  541  TGATGACCAGTTGTTT  556
```